

Polypeptide constructs binding to CD3

[1] The invention relates to a polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3 ϵ chain comprising or consisting of a VH region and a VL region, wherein i) the VH region comprises: a CDR-H1 sequence of X₁YAX₂N, where X₁ is K, V, S, G, R, T, or I; and X₂ is M or I; a CDR-H2 sequence of RIRSKYNNYATYYADX₁VKX₂, where X₁ is S or Q; and X₂ is D, G, K, S, or E; and a CDR-H3 sequence of HX₁NFGNSYX₂SX₃X₄AY, where X₁ is G, R, or A; X₂ is I, L, V, or T; X₃ is Y, W or F; and X₄ is W, F or Y; and ii) wherein the VL region comprises: a CDR-L1 sequence of X₁SSTGAVTX₂X₃X₄YX₅N, where X₁ is G, R, or A; X₂ is S or T; X₃ is G or S; X₄ is N or Y; and X₅ is P or A; a CDR-L2 sequence of X₁TX₂X₃X₄X₅X₆; where X₁ is G or A; X₂ is K, D, or N; X₃ is F, M or K; X₄ is L or R; X₅ is A, P, or V; and X₆ is P or S; and a CDR-L3 sequence of X₁LWYSNX₂WV, where X₁ is V, A, or T; and X₂ is R or L; and iii) wherein one or more of CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one amino acid substitution or a combination thereof selected from X₂4V and X₂4F in CDR-H1; D15, and X₁16A in CDR-H2; H1, X₁2E, F4, and N6 in CDR-H3; and X₁1L and W3 in CDR-L3. The invention also relates to a polynucleotide encoding the polypeptide or polypeptide construct of the invention, a vector comprising said polynucleotide and a host cell transformed or transfected with said polynucleotide or with said vector. Moreover, the invention also provides for a process for the production of said polypeptide or polypeptide construct and a pharmaceutical composition comprising said polypeptide or polypeptide construct of the invention. Furthermore, the invention relates to medical uses of said polypeptide or polypeptide construct and kits comprising said polypeptide or polypeptide construct.

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[2] T cell engagers (TCEs) make use of T cells' ability to recognize foreign peptides on mutated or infected cells through T cell receptors. T cell recognition is mediated by clonotypically distributed alpha beta and gamma delta T cell receptors (TcR) that interact with the peptide-loaded molecules of the peptide MHC (pMHC) at low affinities. The antigen-specific chains of the TcR do not possess signalling domains but instead are coupled to the conserved multisubunit signaling apparatus CD3. The mechanism by which TcR ligation is directly communicated to the signalling apparatus is a fundamental topic of interest in T cell biology. In brief, CD3 subunits that translate cell surface antigen binding into an intracellular phosphorylation signaling cascade. These phosphorylation events culminate in the activation of transcription factors such as NFAT and NFkB that lead to increased expression of cytokines and effector proteins such as granzymes and perforin. It is this characteristic that is used by TCEs which bind simultaneously a target antigen on a tumor cell and CD3 on T cells

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to form an artificial immune synapse eventually leading to the destruction of the cell expressing said target antigen.

[3] From a clinical perspective, TCEs do not only have to show efficient cell killing activity, but at the same time other characteristics like, e.g., a manageable side effect profile are desired. However, these aspects are not the only considerations when it comes to the development of TCEs. Other areas of importance for drug development are pre-patient, i.e. concern characteristics of the TCE outside of the patient's body such as, e.g., shelf life, production scalability, solubility, stability, and ease of formulation. In other terms, an important feature from a pharmaceutical perspective is the developability of a given TCE or parts thereof to address certain needs such as for example in drug production or administration. Bringing together the requirements from clinical and pharmacological perspective is important for TCE platform advancement in relation to commercialization. In view of the biological complexities of having the TCE inducing the formation of the immune synapse, it can be challenging to manipulate the TCE in terms of its other characteristics such as for example shelf life, production scalability, solubility, stability, and ease of formulation while maintaining its effectiveness in mediating the killing of target cells.

[4] Thermal stability of TCEs is an important feature within and outside of the patient's body. A higher thermal stability of TCEs reduces the formation of high molecular weight aggregates caused which in turn provides, e. g., for a TCE that is active for a prolonged time in the body but will also be more stable during storage. Moreover, the reduction of high molecular weight aggregates can also result in a more favourable immunogenetic profile of the TCE upon administration thereby reducing the risk of side effects.

[5] Classically, the VH and VL domains making up the anti-target and anti-CD3 binding domains of TCEs are an area that has been the focus of improving stability. This is in particular true for Fvs that are part of TCEs. The hydrophobic interaction between the VH and the VL is believed to strongly determine the stability of a Fv. The interaction can in many Fvs not be strong enough to be stable for in vitro and/or in vivo applications. This has led to the coupling of the V-domains of an Fv by a linker resulting in single chain Fvs (scFvs). While the linker has shown to be effective in holding the V-domains (variable domains) together, it may not always be effective to keep a scFv active at all or active enough for a given application making it necessary to further improve stability. One approach to increase stability is that by increasing the interaction of the two V-domains, the stability of a biologically active Fv can be increased so that it remains a target binding monomer. Although approaches have been described in the art to improve stability of scFv, there is still a need in the art for improving stability of Fvs that are part of TCEs.

[6] The invention relates to a polypeptide or polypeptide construct comprising:

a binding domain binding to an extracellular epitope of the human CD3 ϵ chain comprising or consisting of a VH region and a VL region, wherein

- i) the VH region comprises:
- 5 a CDR-H1 sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, T, or I; and X_2 is M or I;
- a CDR-H2 sequence of $RIRSKYNNYATYYADX_1VKX_2$, where X_1 is S or Q; and X_2 is D, G, K, S, or E; and
- a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and
- 10 ii) wherein the VL region comprises:
- a CDR-L1 sequence of $X_1SSTGAVTX_2X_3X_4YX_5N$, where X_1 is G, R, or A; X_2 is S or T; X_3 is G or S; X_4 is N or Y; and X_5 is P or A;
- a CDR-L2 sequence of $X_1TX_2X_3X_4X_5X_6$; where X_1 is G or A; X_2 is K, D, or N; X_3 is F, M or K; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S; and
- 15 a CDR-L3 sequence of $X_1LWYSNX_2WV$, where X_1 is V, A, or T; and X_2 is R or L; and
- iii) wherein one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from
- 20 X_24V and X_24F in CDR-H1;
- D15 (preferably E), and X_116A in CDR-H2;
- H1 (preferably A or N), X_12E , F4 (preferably I), and N6 (preferably S or T) in CDR-H3; and
- X_11L and W3 (preferably Y) in CDR-L3.

- 25 **[7]** The term “polypeptide construct” (alternatively referred to also as “compound” herein) refers to an antigen-binding (or epitope-binding) molecule comprising domains themselves comprising paratopes. In the context of the present invention, a polypeptide construct is understood as an organic polymer which comprises at least one continuous, unbranched amino acid chain that naturally is not existing, but was engineered. An example of a
- 30 polypeptide construct that is a single polypeptide is a BiTE[®] molecule that comprises a core structure comprising at least one functional target binding domain together with at least one complete functional CD3 binding domain on a single polypeptide chain, wherein these domains are linked directly by flexible peptide (a “linker”) without any further inserted domain unlike, for example, Xmabs that comprise the target binder and the CD3 binder on different
- 35 polypeptide chains. In the context of the present invention, such a polypeptide construct comprising more than one amino acid chain is likewise envisaged. It is preferred that the term “polypeptide” is used in connection with single chain forms of the compounds of the

present invention, whereas "polypeptide construct" may preferably be more adequate to describe also polypeptides that comprise more than one polypeptide chain, for example two, three or four polypeptide chains. Additionally, the term "polypeptide construct" is also suitable to describe compounds of the invention that comprise one or more non-amino acid-based constituents, e.g. human serum albumin, etc. (HSA). An amino acid chain of a polypeptide typically comprises at least 50 amino acids, preferably at least 100, 200, 300, 400 or 500 amino acids. It is also envisaged in the context of the present invention that an amino acid chain of a polymer is linked to an entity which is not composed of amino acids.

[8] The polypeptides comprise structural and/or functional features based on the structure and/or function of an antibody, e.g., of a full-length immunoglobulin molecule. A polypeptide construct, hence, specifically and, preferably, selectively or immunospecifically binds to its target or antigen, more precisely to an epitope of said target or target antigen, and/or it comprises the heavy chain variable region (VH) and/or the light chain variable region (VL) naturally found in an antibody, or comprises domains derived therefrom. Accordingly, the constructs may alternatively be regarded as comprising paratope-structured and epitope-binding structures, such as those found in natural antibodies or fragments thereof. A polypeptide construct according to the invention comprises the minimum structural requirements of an antibody which allow for immunospecific target binding, i.e., a paratope that recognizes immunospecifically or immunoselectively an epitope on a target antigen unless specified differently. This minimum requirement may e.g. be defined by the presence of at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region, also termed CDR-L1, CDR-L2, and CDR-L3) and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region, also termed CDR-H1, CDR-H2 and CDR-H3), preferably of all six CDRs. A polypeptide construct may hence be characterized by the presence of three or six CDRs in a binding domain, and the skilled person knows where (in which order) those CDRs are located within the paratopic binding structures. In the context of the CD3 binding domain of the polypeptide or polypeptide construct, said paratopic binding structure is specified to be a binding domain characterized by the presence of a VH and VL region comprising CDRs. Hence, a polypeptide/polypeptide construct according to the invention comprises at least a paratopic binding structure being a binding domain binding selectively, immunospecifically and/or immunoselectively to an extracellular epitope of the human CD3ε (also termed CD3epsilon or "CD3 epsilon" herein) chain comprising VH and VL regions with CDRs. Accordingly, a polypeptide/polypeptide construct according to the invention comprises a paratope selectively, immunospecifically and/or immunoselectively binding to an epitope of human CD3 epsilon. The terms "CDR", and its plural "CDRs", refer to the complementarity determining region of which three make up the binding character of a light chain variable region (CDR-L1, CDR-L2 and CDR-L3) and three make up the binding character of a heavy

chain variable region (CDR-H1, CDR-H2 and CDR-H3). CDRs contain most of the residues responsible for specific interactions of antibodies (or constructs or binding domain) with an antigen and hence contribute to the functional activity of an antibody molecule: they are the main determinants of antigen specificity. The exact definition of CDR boundaries and lengths is subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or any other boundary definitions, including the numbering system described herein. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See for example Kabat (an approach based on cross-species sequence variability), Chothia (an approach based on crystallographic studies of antigen-antibody complexes), and/or MacCallum (Kabat et al., loc. cit.; Chothia et al., J. Mol. Biol, 1987, 196: 901-917; and MacCallum et al., J. Mol. Biol, 1996, 262: 732). Still another standard for characterizing the antigen binding site is the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, e.g., Protein Sequence and Structure Analysis of Antibody Variable Domains. In: Antibody Engineering Lab Manual (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg). To the extent that two residue identification techniques define regions of overlapping, but not identical regions, they can be combined to define a hybrid CDR. However, the numbering in accordance with the so-called Kabat system is preferred. The term "antigen-binding structure", as used herein, refers to any polypeptide/polypeptide construct that comprises an antigen-binding structure or any molecule that has binding activity to a specified antigen. Said antigen-binding structures or molecules are not limited to those derived from a living organism, and for example, they may be a polypeptide produced from an artificially designed sequence. They may also be any of a naturally occurring polypeptide, synthetic polypeptide, recombinant polypeptide, and such. As the antigen-binding structure in accordance with the present invention bind specifically to parts of an antigen, i.e., they bind specifically to an epitope of CD3epsilon, the antigen (epitope)-binding structure may also be broadly defined as "paratopic structure" herein. Accordingly, the polypeptides/polypeptide constructs according to the invention may also be defined as a domain comprising a paratope that are preferably immunospecifically or immunoselectively binding to a target antigen/target epitope; and in certain embodiments comprising at least a further paratope, preferably immunospecifically or immunoselectively, binding to a further, different or same, target antigen/target epitope. Therefore, whenever the present description refers to a domain of a construct or molecule of the present invention, the construct comprises at least one paratopic structure (or paratope) binding human CD3epsilon as specified herein, particularly according to any one of the appended claims. In certain embodiments, said construct comprises at

least a further paratope binding also to human CD3epsilon or a different target antigen as defined herein.

[9] The term “antibody” as used in accordance with the invention comprises full-length antibodies, also including camelid antibodies and other immunoglobulins generated by biotechnological or protein engineering methods or processes. These full-length antibodies may be for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies, as well as antibodies from other species such as mouse, hamster, rabbit, rat, goat, or non-human primates.

[10] “Polypeptides/polypeptide constructs” of the present invention may also comprise the structure of a full-length immunoglobulin as it occurs naturally. For example, they may comprise (at least) two full-length antibody heavy chains and two full-length antibody light chains. However, given that the polypeptides/polypeptide constructs according to the invention preferably comprise a linker linking the VH and VL region of the CD3 binding domain, preferably resulting in a scFv, and/or, in other embodiments, comprise at least one further binding domain comprising a paratope, they do not occur naturally, and they are markedly different in their function from naturally occurring products. A polypeptide or polypeptide construct of the invention is hence an artificial “hybrid” molecule comprising, preferably, an scFv and/or, in some embodiments, distinct paratopes/binding domains with different specificities and/or selectivities.

[11] As indicated above, the polypeptides of the invention may comprise more than one polypeptide chain, i.e. polypeptides comprising two or more polypeptide chains are also subject to the present invention, particularly polypeptides forming a three-dimensional protein-like structure that allows for the immunospecific binding to CD3epsilon. Therefore, the definition of the term “polypeptide construct” includes molecules consisting of only one polypeptide chain as well as molecules consisting of two, three, four or more polypeptide chains, which chains can be either identical (homodimers, homotrimers or homo oligomers) or different (heterodimer, heterotrimer or heterooligomer). Examples for the above identified antibodies and their fragments, variants, derivatives and constructs derived therefrom are described inter alia in Harlow and Lane, Antibodies: A laboratory manual, CSHL Press (1988); Kontermann and Dübel, Antibody Engineering, Springer, 2nd ed. 2010; and Little, Recombinant Antibodies for Immunotherapy, Cambridge University Press 2009.

[12] “Polypeptides/polypeptide constructs” of the present invention may also comprise fragments of full-length antibodies, such as VH, VHH, VL, (s)dAb, Fv, light chain (VL-CL), Fd (VH-CH1), heavy chain, Fab, Fab', F(ab')₂ or “rlgG” (“half antibody” consisting of a heavy chain and a light chain), whereas not all of the foregoing fragments are applicable for the CD3epsilon binding domain since it is defined to comprise a VH and a VL region, but to the

embodiments regarding the at least one further binding domain. Polypeptides/polypeptide constructs according to the invention may also comprise modified fragments of antibodies, also called antibody variants or antibody derivatives. Examples include, but are not limited to, scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab2, Fab3, diabodies, single chain

5 diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, „minibodies“ exemplified by a structure which is as follows: (VH-VL-CH3)2, (scFv-CH3)2, ((scFv)2-CH3 + CH3), ((scFv)2-CH3) or (scFv-CH3-scFv)2, multibodies such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable region, which might be VHH, VH or VL, that selectively and,

10 preferably, specifically binds to an antigen or target independently of other variable regions or domains, whereas not all of the foregoing fragments are applicable for the CD3epsilon binding domain since it is defined to comprise a VH and a VL region, but to the embodiments regarding the at least one further binding domain. Further possible formats of the polypeptides/polypeptide constructs according to the invention are cross bodies, maxi

15 bodies, hetero Fc constructs, mono Fc constructs and scFc constructs. Examples for those formats will be described herein below.

[13] Furthermore, the definition of the term “polypeptide construct” includes bivalent and polyvalent / multivalent polypeptides/polypeptide constructs as well as bispecific and polyspecific / multispecific polypeptides/polypeptide constructs, which selectively and,

20 preferably, specifically bind to two, three or more antigenic structures (epitopes), through distinct binding domains. A polypeptide construct can have more binding valences than specificities, e.g. in a case where it has two binding domains for one target (CD3epsilon) and one binding domain for another target, for example those described herein below, or vice versa, in which case the polypeptide construct is trivalent and bispecific. In general, the term

25 “bispecific” includes the meaning that a polypeptide construct binds to at least two different antigens, such as said CD3epsilon and a further target, for example those specified herein below.

[14] The terms “paratope”, “antigen-binding domain”, “epitope-binding domain”, “binding domain” or “domain which binds to...” characterize, in connection with the present invention,

30 a domain of the construct which selectively and, preferably, specifically or immunospecifically binds to / interacts with / recognizes an epitope on the target or antigen (here: CD3). The terms “binding domain” or “domain which binds to...” or “domain” as far as it relates to the herein described “constructs” characterizes in connection with the present invention a domain of the construct which immunospecifically binds to / interacts with / recognizes an

35 epitope on the target or antigen. The structure and function of the CD3epsilon binding domain (also termed as first binding domain in the case of a polypeptide/polypeptide construct comprising a further, consequently second, third, and so on, binding domain), and

preferably also the structure and/or function of any further binding domain (binding to for example to a cell surface antigen such as a tumor antigen), is/are based on the structure and/or function of an antibody, e.g. of a full-length immunoglobulin polypeptide. The "binding domain" or "domain which binds to..." may hence comprise the minimum structural requirements of an antibody which allow for immunospecific target binding. While the structural requirements of the CD3epsilon binding domain is specified to comprise a VH and VL region with corresponding three CDRs per region, said minimum structural requirement in any further binding domain may e.g. be defined by the presence of at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or of three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region), preferably of all six CDRs. A "domain which binds to" (or a "binding domain") may typically comprise an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH); however, it does not have to comprise both, but may comprise only one of VH or VL. Fd fragments, for example, often retain some antigen-binding function of the intact antigen-binding domain. The terms "paratope", "antigen-binding structure" and "epitope-binding structure, as used herein, refer also to a portion of an antibody (or a molecule according to the invention), which comprises a region that specifically binds and is complementary to the whole or a portion of an antigen or a part thereof, i.e. an antibody can only bind to a particular portion of the antigen. The particular portion is called "epitope". An antigen-binding domain can be provided from one or more antibody variable domains. Preferably, the antigen-binding domains contain antibody variable region that comprising both the antibody light chain variable region (VL) and antibody heavy chain variable region (VH). Such preferable antigen-binding domains include, for example, "single-chain Fv (scFv)", "single-chain antibody", "Fv", "single-chain Fv2 (scFv2)", "Fab", and "F (ab')₂". For the CD3epsilon binding domain it is preferred that it takes the form of an scFv.

[15] Examples for the format of a "domain which binds to", "domain comprising a paratope"(or "binding domain", "antigen-binding structure", "epitope-binding structure") include unless otherwise defined, but are not limited to, full-length antibodies, fragments of full-length antibodies (such as VH, VHH, VL), (s)dAb, Fv, light chain (VL-CL), Fd (VH-CH1), heavy chain, Fab, Fab', F(ab')₂ or "r IgG" ("half antibody")), antibody variants or derivatives such as scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab2, Fab3, diabodies, single chain diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, „minibodies“ (selected from formats such as (VH-VL-CH3)₂, (scFv-CH3)₂, ((scFv)₂-CH3 + CH3)), ((scFv)₂-CH3) or (scFv-CH3-scFv)₂, multibodies such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable region, which might be VHH, VH or VL. Further examples for the format of a "domain which binds to" (or a "binding domain") include (1) an antibody

fragment or variant comprising VL, VH, CL and CH1 (such as Fab); (2) an antibody fragment or variant comprising two linked Fab fragments (such as a F(ab')₂); (3) an antibody fragment or variant comprising VH and CH1 (such as Fd); (4) an antibody fragment or variant comprising VL and CL (such as the light chain); (5) an antibody fragment or variant comprising VL and VH (such as Fv); (5) a dAb fragment (Ward et al., (1989) Nature 341 :544-546), which has a VH domain; (6) an antibody variant comprising at least three isolated CDRs of the heavy and/or the light chain; and (7) a single chain Fv (scFv). Examples for embodiments of constructs or binding domains according to the invention are e.g. described in WO 00/006605, WO 2005/040220, WO 2008/119567, WO 2010/037838, WO 2013/026837, WO 2013/026833, US 2014/0308285, US 2014/0302037, WO 2014/144722, WO 2014/151910, and WO 2015/048272. In the context of the present invention, a paratope is understood as an antigen-binding site which is a part of a polypeptide as described herein and which recognizes and binds to an antigen. A paratope is typically a small region of about at least 5 amino acids. A paratope as understood herein typically comprises parts of antibody-derived heavy (VH) and light chain (VL) sequences. Each binding domain of a polypeptide according to the present invention is provided with a paratope comprising a set of 6 complementarity-determining regions (CDR loops) with three of each being comprised within the antibody-derived VH and VL sequence, respectively.

[16] It is envisaged for the compounds, particularly for the constructs of the present invention that a) the construct is a single chain polypeptide or a single chain construct, b) the CD3epsilon binding domain is in the format of an scFv, c) any further, such as a second binding and/or third domain is in the format of an scFv, d) the first and said further, such as said second and/or third domain are connected via a linker, preferably a peptide linker, more preferably a glycine/serine or glycine/glutamine linker, and/or e) the construct comprises a domain providing an extended serum half-life, such as an Fc-based domain, or human serum albumin (HSA). In the latter case, it is a preferred embodiment, wherein the term "polypeptide construct" makes clear that it comprises more than a single peptide chain. A preferred Fc-based domain which extends the serum half-life (also termed "HLE" domain) comprises two polypeptide monomers, each comprising a hinge, a CH2 domain and a CH3 domain, wherein said two polypeptide monomers are fused to each other via a peptide linker (see, e.g., SEQ ID NO: 18 and 19); the format is in N-terminal to C-terminal order: hinge-CH2-CH3-linker-hinge-CH2-CH3.

[17] The constructs of the present invention are preferably "in vitro generated constructs" and/or "recombinant constructs". In the context of the present invention, the term "in vitro generated" refers to a construct according to the above definition where all or part of the binding domain or of a variable region (e.g., at least one CDR) is generated in a non-immune cell selection, e.g., in an in vitro phage display, on a protein chip or in any other method in

which candidate amino acid sequences can be tested for their ability to bind to an antigen. This term thus preferably excludes sequences generated solely by genomic rearrangement in an immune cell in an animal. It is envisaged that the first and/or second domain of the construct is produced by or obtainable by phage display or library screening methods rather than by grafting CDR sequences from a pre-existing (monoclonal) antibody into a scaffold. A
5 "recombinant construct" is a construct generated or produced using (inter alia) recombinant DNA technology or genetic engineering.

[18] The constructs of the present invention are envisaged to be monoclonal. As used herein, polypeptides or constructs that are denominated "monoclonal" (mAb) are obtained
10 from a population of substantially homogeneous antibodies / constructs, i.e., the individual antibodies / constructs comprised in the population are identical (in particular with respect to their amino acid sequence) except for possible naturally occurring mutations and/or post-translational modifications (e.g., isomerizations, amidations) that may be present in minor amounts. Monoclonal antibodies / constructs are highly specific, being directed against a
15 single epitope within the antigen, in contrast to polyclonal antibody preparations which typically include different antibodies directed against different determinants (or epitopes). In addition to their specificity, monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, hence uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody / construct as being obtained
20 from a substantially homogeneous population of antibodies and is not to be construed as requiring production of the antibody by any specific method.

[19] For the preparation of monoclonal antibodies, any technique providing antibodies produced by continuous cell line cultures can be used. For example, monoclonal antibodies to be used may be made by the hybridoma method first described by Koehler et al., Nature,
25 256: 495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567). Examples for further techniques to produce human monoclonal antibodies include the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96).

[20] Hybridomas can then be screened using standard methods, such as enzyme-linked immunosorbent assay (ELISA) and surface plasmon resonance (BIAcore™) analysis, to identify one or more hybridomas that produce an antibody that selectively and, preferably, specifically or immunospecifically binds to a specified antigen. Any form of the relevant antigen may be used as the immunogen, e.g., recombinant antigen, naturally occurring
35 forms, any variants or fragments thereof, as well as an antigenic peptide thereof. Surface plasmon resonance as employed in the BIAcore™ system can be used to increase the

efficiency of phage antibodies / constructs which bind to an epitope of a target antigen (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmberg, J. Immunol. Methods 183 (1995), 7-13).

5 [21] Another exemplary method of making constructs or binding domains includes screening protein expression libraries, e.g., phage display or ribosome display libraries. Phage display is described, for example, in Ladner et al., U.S. Patent No. 5,223,409; Smith (1985) Science 228:1315-1317, Clackson et al., Nature, 352: 624-628 (1991) and Marks et al., J. Mol. Biol., 222: 581-597 (1991).

10 [22] In addition to the use of display libraries, the relevant antigen can be used to immunize a non-human animal, e.g., a rodent (such as a mouse, hamster, rabbit or rat). In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig (immunoglobulin) loci. Using the hybridoma technology, antigen-specific monoclonal antibodies derived from the genes with the desired
15 specificity may be produced and selected. See, e.g., Xenomouse™ mouse, Green et al. (1994) Nature Genetics 7:13-21, US 2003-0070185, WO 96/34096, and WO 96/33735.

[23] A monoclonal antibody can also be obtained from a non-human animal, and then modified, e.g., humanized, deimmunized, rendered chimeric etc., using recombinant DNA techniques known in the art. Examples of modified constructs or binding domains include
20 humanized variants of non-human antibodies / constructs, "affinity matured" constructs or binding domains (see, e.g. Hawkins et al. J. Mol. Biol. 254, 889-896 (1992) and Lowman et al., Biochemistry 30, 10832- 10837 (1991)) and antibody variants or mutants with altered effector function(s) (see, e.g., US Patent 5,648,260, Kontermann and Dübel (2010), loc. cit. and Little (2009), loc. cit.).

25 [24] In immunology, affinity maturation is the process by which B cells produce antibodies with increased affinity for antigen during the course of an immune response. With repeated exposures to the same antigen, a host will produce antibodies of successively greater affinities. Like the natural prototype, the in vitro affinity maturation is based on the principles of mutation and selection. The in vitro affinity maturation has successfully been used to
30 optimize antibodies, antibody fragments, antibody variants, constructs or binding domains. Random mutations inside the CDRs are introduced using radiation, chemical mutagens or error-prone PCR. In addition, the genetic diversity can be increased by chain shuffling. Two or three rounds of mutation and selection using display methods like phage display usually results in antibodies, antibody fragments, antibody variants, constructs or binding domains
35 with affinities in the low nanomolar range.

[25] A preferred type of an amino acid substitutional variation of the constructs or binding domains of the invention involves substituting one or more residues within the hypervariable region of a parent antibody structure (e.g. a humanized or human antibody structure). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody structure from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several sites of the hypervariable region (e. g. 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e.g. binding affinity) as disclosed herein. To identify candidate hypervariable region sites contributing significantly to antigen binding (candidates for modification), alanine scanning mutagenesis can also be performed. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the complex between the antigen and the construct or the binding domain to identify contact points between the binding domain and its specific antigen. Such contact residues and neighbouring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies, their antigen-binding fragments, constructs or binding domains with superior properties in one or more relevant assays may be selected for further development.

[26] The constructs and binding domains of the present invention specifically include "chimeric" versions in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments or variants of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; Morrison et al., Proc. Natl. Acad. Sci. USA, 81: 6851-6855 (1984)). Chimeric constructs or binding domains of interest herein include "primitized" constructs comprising variable domain antigen-binding sequences derived from a non-human primate (e.g., Old World Monkey, Ape etc.) and human constant region sequences. A variety of approaches for making chimeric antibodies or constructs have been described. See e.g., Morrison et al., Proc. Natl. Acad. Sci. U.S.A. 81:6851, 1985; Takeda et al., Nature 314:452, 1985, Cabilly et al., U.S. Patent No. 4,816,567; Boss et al., U.S. Patent No. 4,816,397; Tanaguchi et al., EP 0171496; EP 0173494; and GB 2177096.

[27] An antibody, polypeptide construct, antibody fragment, antibody variant or binding domain may also be modified by specific deletion of human T cell epitopes (a method called “deimmunization”) using methods disclosed for example in WO 98/52976 or WO 00/34317. Briefly, the heavy and light chain variable regions of an antibody, construct or binding domain can be analyzed for peptides that bind to MHC class II; these peptides represent potential T cell epitopes (as defined e.g. in WO 98/52976 and WO 00/34317). For detection of potential T cell epitopes, a computer modeling approach termed “peptide threading” can be applied, and in addition a database of human MHC class II binding peptides can be searched for motifs present in the VH and VL sequences, as described in WO 98/52976 and WO 00/34317. These motifs bind to any of the 18 major MHC class II DR allotypes, and thus constitute potential T cell epitopes. Potential T cell epitopes detected can be eliminated by substituting small numbers of amino acid residues in the variable domains or variable regions, or preferably, by single amino acid substitutions. Typically, conservative substitutions are made. Often, but not exclusively, an amino acid common to a position in human germline antibody sequences may be used. Human germline sequences are disclosed e.g. in Tomlinson, et al. (1992) J. Mol. Biol. 227:776-798; Cook, G.P. et al. (1995) Immunol. Today Vol. 16 (5): 237-242; and Tomlinson et al. (1995) EMBO J. 14: 14:4628-4638. The V BASE directory (www2.mrc-lmb.cam.ac.uk/vbase/list2.php) provides a comprehensive directory of human immunoglobulin variable region sequences (compiled by Tomlinson, LA. et al. MRC Centre for Protein Engineering, Cambridge, UK). These sequences can be used as a source of human sequence, e.g., for framework regions and CDRs. Consensus human framework regions can also be used, for example as described in US Patent No. 6,300,064.

[28] “Humanized” antibodies, variants or fragments thereof, constructs and binding domains are based on immunoglobulins of mostly human sequences, which contain (a) minimal sequence(s) derived from non-human immunoglobulin. For the most part, humanized antibodies, variants or fragments thereof, constructs and binding domains are based on human immunoglobulins (recipient antibodies) in which residues from a hypervariable region or CDR are replaced by residues from a hypervariable region or CDR of a non-human species (donor antibody) such as a rodent (e.g. mouse, hamster, rat or rabbit) having the desired specificity, affinity, capacity and/or biological activity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, “humanized” antibodies, variants or fragments thereof, constructs and binding domains as used herein may also comprise residues which are found neither in the recipient antibody nor the donor antibody. These modifications are made to further refine and optimize antibody performance. The humanized antibodies, variants or fragments thereof, constructs and binding domains may also comprise

at least a portion of an immunoglobulin constant region (such as Fc), typically that of a human immunoglobulin. For further details, see Jones et al., *Nature*, 321: 522-525 (1986); Reichmann et al., *Nature*, 332: 323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2: 593-596 (1992).

5 **[29]** Humanized antibodies, variants or fragments thereof, constructs and binding domains can be generated by replacing sequences of the (Fv) variable region that are not directly involved in antigen binding with equivalent sequences from human (Fv) variable regions. Exemplary methods for generating such molecules are provided by Morrison (1985) *Science* 229:1202-1207; by Oi et al. (1986) *BioTechniques* 4:214; and by US 5,585,089;
10 US 5,693,761; US 5,693,762; US 5,859,205; and US 6,407,213. These methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin (Fv) variable regions from at least one of a heavy or light chain. Such nucleic acids may be obtained from a hybridoma producing an antibody against a predetermined target, as described above, as well as from other sources. The recombinant DNA encoding
15 the humanized antibody, variant or fragment thereof, construct or binding domain can then be cloned into an appropriate expression vector.

[30] Humanized antibodies, variants or fragments thereof, constructs and binding domains may also be produced using transgenic animals such as mice that express human heavy and light chain genes but are incapable of expressing the endogenous mouse immunoglobulin
20 heavy and light chain genes. Winter describes an exemplary CDR grafting method that may be used to prepare the humanized molecules described herein (U.S. Patent No. 5,225,539). All the CDRs of a given human sequence may be replaced with at least a portion of a non-human CDR, or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the number of CDRs required for binding of the humanized molecule to
25 a predetermined antigen.

[31] A humanized antibody, variant or fragment thereof, construct or binding domain can be optimized by the introduction of conservative substitutions, consensus sequence substitutions, germline substitutions and/or back mutations. Such altered immunoglobulin molecules can be made by any of several techniques known in the art, (e.g., Teng et al.,
30 *Proc. Natl. Acad. Sci. U.S.A.*, 80: 7308-7312, 1983; Kozbor et al., *Immunology Today*, 4: 7279, 1983; Olsson et al., *Meth. Enzymol.*, 92: 3-16, 1982, and EP 239 400).

[32] Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies / constructs. It is however expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or
35 multi-dose utilizations of an antibody or construct. Thus, it would be desirable to provide

constructs comprising a human binding domain against a target, to vitiate concerns and/or effects of HAMA or HACA response.

[33] Therefore, according to one embodiment, the polypeptide construct having at least one further binding domain, said binding domain(s) are "human". The term "human antibody",
5 "human construct" and "human binding domain" includes antibodies, constructs and binding domains, respectively, having antibody-derived regions such as variable and constant regions or domains which correspond substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat et al. (1991) (loc. cit.). The human constructs or binding domains of the invention may include amino acid
10 residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs, and particularly in CDR3. The human constructs or binding domains can have at least one, two, three, four, five, or more positions replaced with an amino acid residue that is not encoded by the human germline immunoglobulin sequence. The definition
15 of human antibodies, constructs and binding domains as used herein also contemplates fully human antibodies, constructs and binding domains which include only non-artificially and/or genetically altered human sequences of antibodies as those can be derived by using technologies or systems such as the XenomouseTM mouse.

[34] Polypeptides/polypeptide constructs comprising at least one human binding domain
20 may avoid some of the problems associated with antibodies or constructs that possess non-human such as rodent (e.g. murine, rat, hamster or rabbit) variable and/or constant regions. The presence of such rodent derived proteins can lead to the rapid clearance of the antibodies or constructs or can lead to the generation of an immune response against the antibody or construct by a patient. To avoid the use of rodent-derived constructs, humanized
25 or fully human constructs can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies.

[35] The ability to clone and reconstruct megabase-sized human loci in YACs and to introduce them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci as well as generating useful
30 models of human disease. Furthermore, the use of such technology for substitution of mouse loci with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression.

[36] An important practical application of such a strategy is the "humanization" of the
35 mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated offers the opportunity to study the

mechanisms underlying programmed expression and assembly of antibodies as well as their role in B-cell development. Furthermore, such a strategy could provide an ideal source for production of fully human monoclonal antibodies (mAbs) – an important milestone towards fulfilling the promise of antibody therapy in human disease. Fully human antibodies or
5 constructs derived therefrom are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies / constructs. The use of fully human antibodies or constructs can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as inflammation, autoimmunity, and cancer, which
10 require repeated compound administrations.

[37] One approach towards this goal was to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the
15 proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human mAbs with the desired specificity could be
20 readily produced and selected. This general strategy was demonstrated in connection with the generation of the first XenoMouse™ mouse strains (see Green et al. Nature Genetics 7:13-21 (1994)). The XenoMouse™ strains were engineered with yeast artificial chromosomes (YACs) containing 245 kb and 190 kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained
25 core variable and constant region sequences. The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human mAbs. These results also
30 suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions might recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was extended to the introduction of greater than approximately 80% of the human antibody repertoire through
35 introduction of megabase sized, germline configuration YAC fragments of the human heavy chain loci and kappa light chain loci, respectively. See Mendez et al. Nature Genetics 15:146-156 (1997) and U.S. patent application Ser. No. 08/759,620.

[38] The production of the XenoMouse™ model is further discussed and delineated in U.S. patent applications Ser. No. 07/466,008, Ser. No. 07/610,515, Ser. No. 07/919,297, Ser. No. 07/922,649, Ser. No. 08/031,801, Ser. No. 08/112,848, Ser. No. 08/234,145, Ser. No. 08/376,279, Ser. No. 08/430,938, Ser. No. 08/464,584, Ser. No. 08/464,582, 5 Ser. No. 08/463,191, Ser. No. 08/462,837, Ser. No. 08/486,853, Ser. No. 08/486,857, Ser. No. 08/486,859, Ser. No. 08/462,513, Ser. No. 08/724,752, Ser. No. 08/759,620; and U.S. Pat. Nos. 6,162,963; 6,150,584; 6,114,598; 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also Mendez et al. Nature Genetics 15:146-156 (1997) and Green and Jakobovits J. Exp. Med. 188:483-495 (1998), 10 EP 0 463 151 B1, WO 94/02602, WO 96/34096, WO 98/24893, WO 00/76310, and WO 03/47336.

[39] In an alternative approach, others, including GenPharm International, Inc., have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or 15 more VH genes, one or more DH genes, one or more JH genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani et al. and U.S. Pat. Nos. 5,545,806; 5,625,825; 5,625,126; 5,633,425; 5,661,016; 5,770,429; 5,789,650; 5,814,318; 5,877,397; 5,874,299; and 6,255,458 each to Lonberg and Kay, 20 U.S. Pat. Nos. 5,591,669 and 6,023,010 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205; 5,721,367; and 5,789,215 to Berns et al., and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, Ser. No. 07/575,962, Ser. No. 07/810,279, Ser. No. 07/853,408, Ser. No. 07/904,068, Ser. No. 07/990,860, Ser. No. 08/053,131, Ser. No. 08/096,762, Ser. No. 08/155,301, Ser. No. 08/161,739, 25 Ser. No. 08/165,699, Ser. No. 08/209,741. See also EP 0 546 073 B1, WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175. See further Taylor et al. (1992), Chen et al. (1993), Tuaillon et al. (1993), Choi et al. (1993), Lonberg et al. (1994), Taylor et al. (1994), and Tuaillon et al. (1995), Fishwild et al. (1996).

30 [40] Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. See European Patent Application Nos. 773 288 and 843 961. Xenerex Biosciences is developing a technology for the potential generation of human antibodies. In this technology, SCID mice are reconstituted with human lymphatic cells, e.g., B and/or 35 T cells. Mice are then immunized with an antigen and can generate an immune response against the antigen. See U.S. Pat. Nos. 5,476,996; 5,698,767; and 5,958,765.

[41] In some embodiments, the constructs of the invention are “isolated” or “substantially pure” constructs. “Isolated” or “substantially pure”, when used to describe the constructs disclosed herein, means a construct that has been identified, separated and/or recovered from a component of its production environment. Preferably, the construct is free or substantially free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that could interfere with diagnostic or therapeutic uses for the construct, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous compounds. It is understood that the isolated or substantially pure construct may constitute from 5% to 99.9% by weight of the total protein / polypeptide content in a given sample, depending on the circumstances. The desired construct may be produced at a significantly higher concentration using an inducible promoter or high expression promoter. The definition includes the production of a construct in a wide variety of organisms and/or host cells that are known in the art. In certain embodiments, the construct will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie Blue or, preferably, silver staining. Usually, however, an isolated construct will be prepared by at least one purification step.

[42] According to one embodiment, the entire construct and/or the binding domains are in the form of one or more polypeptides or in the form of proteins. In addition to proteinaceous parts, such polypeptides or proteins may include non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde).

[43] Peptides are short chains of amino acid monomers linked by covalent peptide (amide) bonds. Hence, peptides fall under the broad chemical classes of biological oligomers and polymers. Amino acids that are part of a peptide or polypeptide chain are termed “residues” and can be consecutively numbered. All peptides except cyclic peptides have an N-terminal residue at one end and a C-terminal residue at the other end of the peptide. An oligopeptide consists of only a few amino acids (usually between two and twenty). A polypeptide is a longer, continuous, and unbranched peptide chain. Peptides are distinguished from proteins based on size, and as an arbitrary benchmark can be understood to contain approximately 50 or fewer amino acids. Proteins consist of one or more polypeptides, usually arranged in a biologically functional way. While aspects of the lab techniques applied to peptides versus polypeptides and proteins differ (e.g., the specifics of electrophoresis, chromatography, etc.), the size boundaries that distinguish peptides from polypeptides and proteins are not absolute. Therefore, in the context of the present invention,

the terms “peptide”, “polypeptide” and “protein” may be used interchangeably, and the term “polypeptide” is often preferred.

[44] Polypeptides may further form multimers such as dimers, trimers and higher oligomers, which consist of more than one polypeptide molecule, as mentioned above.

5 Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding structures of higher order of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a heteromultimer is an antibody or immunoglobulin molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms
10 “peptide”, “polypeptide” and “protein” also refer to naturally modified peptides / polypeptides / proteins wherein the modification is accomplished e.g. by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. A “peptide”, “polypeptide” or “protein” when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art and described herein below.

15 **[45]** The terms “selectively” and, “preferably, selectively”, “(specifically or immunospecifically) binds to”, “(specifically or immunospecifically) recognizes”, or “(specifically or immunospecifically) reacts with” mean in accordance with this invention that a construct or a binding domain selectively interacts or (immuno-)specifically interacts with a given epitope on the target molecule (antigen), here: CD3, respectively. This selective
20 interaction or association occurs more frequently, more rapidly, with greater duration, with greater affinity, or with some combination of these parameters, to an epitope on the specific target (here: CD3epsilon) than to alternative substances (non-target molecules, e.g., here CD3gamma, etc.). Because of the sequence similarity between homologous proteins in different species, a construct or a binding domain that selectively and/or immunospecifically
25 binds to its target (such as a human target) may, however, cross-react with homologous target molecules from different species (such as, from non-human primates). The terms “selectively binds to”, “specific / immunospecific binding”, etc. can hence include the binding of a construct or binding domain to epitopes or structurally related epitopes in more than one species. In the context of the present invention, a polypeptide of the present invention binds
30 to its respective target structure in a particular manner. Preferably, a polypeptide according to the present invention comprises one paratope per binding domain which specifically or immunospecifically binds to”, “(specifically or immunospecifically) recognizes”, or “(specifically or immunospecifically) reacts with” its respective target structure. This means in accordance with this invention that a polypeptide or a binding domain thereof interacts or
35 (immuno-)specifically interacts with a given epitope on the target molecule (antigen), namely CD3epsilon, and in certain embodiments with a given epitope on at least one further, such as a second and/or a third target molecule. This interaction or association occurs more

frequently, more rapidly, with greater duration, with greater affinity, or with some combination of these parameters, to an epitope on the specific target than to alternative substances (non-target molecules). Because of the sequence similarity between homologous proteins in different species, an antibody construct or a binding domain that immunospecifically binds to its target (such as a human target) may, however, cross-react with homologous target molecules from different species (such as, from non-human primates). The term “specific / immunospecific binding” can hence include the binding of an antibody construct or binding domain to epitopes and/or structurally related epitopes in more than one species. The term “(immuno-) selectively binds does exclude the binding to structurally related epitopes.

10 **[46]** In the context of the present invention, the term “epitope” refers to the part or region of the antigen that is selectively recognized / immunospecifically recognized by the binding structure, i.e. the paratope. An “epitope” is antigenic, and thus the term epitope is sometimes also referred to as “antigenic structure” or “antigenic determinant”. The part of the binding domain that binds to the epitope is called a paratope. Specific binding is believed to be
15 accomplished by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved because of their primary, secondary and/or tertiary structure as well as the result of potential secondary modifications of said structures. The specific interaction of the paratope with its antigenic determinant may result in a simple binding of said site to the antigen. In some cases, the specific interaction may alternatively or
20 additionally result in the initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

[47] The epitopes of protein antigens are divided into two categories, conformational epitopes and linear epitopes, based on their structure and interaction with the paratope. A conformational epitope is composed of discontinuous sections of the antigen's amino acid
25 sequence. These epitopes interact with the paratope based on the three-dimensional surface features and shape or tertiary structure (folding) of the antigen. Methods of determining the conformation of epitopes include, but are not limited to, x-ray crystallography, two-dimensional nuclear magnetic resonance (2D-NMR) spectroscopy and site-directed spin labelling and electron paramagnetic resonance (EPR) spectroscopy. By contrast, linear
30 epitopes interact with the paratope based on their primary structure. A linear epitope is formed by a continuous sequence of amino acids from the antigen and typically includes at least 3 or at least 4, and more usually, at least 5 or at least 6 or at least 7, for example, about 8 to about 10 amino acids in a unique sequence.

[48] A method for epitope mapping for a given human target protein is described in the
35 following: A pre-defined region (a contiguous amino acid stretch) within said given human target protein is exchanged / replaced with a corresponding region of a target protein

paralogue (so long as the binding domain is not cross-reactive with the paralogue used). These human target / paralogue chimeras are expressed on the surface of host cells (such as CHO cells). Binding of the antibody or construct can be tested via FACS analysis. When the binding of the antibody or construct to the chimeric molecule is entirely abolished, or
5 when a significant binding decrease is observed, it can be concluded that the region of human target which was removed from this chimeric molecule is relevant for the immunospecific epitope-paratope recognition. Said decrease in binding is preferably at least 10%, 20%, 30%, 40%, or 50%; more preferably at least 60%, 70%, or 80%, and most preferably 90%, 95% or even 100% in comparison to the binding to human (wild-type) target,
10 whereby binding to the human target is set to be 100%. Alternatively, the above described epitope mapping analysis can be modified by introducing one or several point mutations into the sequence of the human target. These point mutations can e.g. reflect the differences between the human target and its paralogue.

[49] A further method to determine the contribution of a specific residue of a target antigen
15 to the recognition by a construct or binding domain is alanine scanning (see e.g. Morrison KL & Weiss GA. Curr Opin Chem Biol. 2001 Jun;5(3):302-7), where each residue to be analyzed is replaced by alanine, e.g. via site-directed mutagenesis. Alanine is used because of its non-bulky, chemically inert, methyl functional group that nevertheless mimics the secondary structure references that many of the other amino acids possess. Sometimes bulky amino
20 acids such as valine or leucine can be used in cases where conservation of the size of mutated residues is desired.

[50] The interaction between the binding domain and the epitope of the target antigen implies that a binding domain exhibits appreciable or significant affinity for the epitope / the target antigen (here: CD3) and, generally, does not exhibit significant affinity for proteins or
25 antigens other than the target antigen – notwithstanding the above discussed cross-reactivity with homologous targets e.g. from other species. “Significant affinity” includes binding with an affinity (dissociation constant, KD) of $\leq 10^{-6}$ M. Preferably, binding is considered specific when the binding affinity is $\leq 10^{-7}$ M, $\leq 10^{-8}$ M, $\leq 10^{-9}$ M, $\leq 10^{-10}$ M, or even $\leq 10^{-11}$ M, or $\leq 10^{-12}$ M. Whether a binding domain (immuno-)specifically reacts with or binds to a target can be
30 tested readily e.g. by comparing the affinity of said binding domain to its desired target protein or antigen with the affinity of said binding domain to non-target proteins or antigens (here: proteins other than CD3). Preferably, a construct of the invention does not significantly bind to proteins or antigens other than CD3 (i.e., the CD3 binding domain does not bind to proteins other than CD3) – unless any further binding domain(s) directed against a further
35 target is/are deliberately introduced into the construct of the invention, in which case the binding of that binding domain to its specific target is also provided by the present invention.

[51] It is envisaged that the affinity of the first domain for human CD3epsilon is ≤ 100 nM, ≤ 90 nM, ≤ 80 nM, ≤ 70 nM, ≤ 60 nM, ≤ 50 nM, ≤ 40 nM, ≤ 30 nM, or ≤ 20 nM. These values are preferably measured in a cell-based assay, such as a Scatchard assay. Other methods of determining the affinity are also well-known. These values are preferably measured in a surface plasmon resonance assay, such as a Biacore assay.

[52] The term "does not significantly bind" and "does not selectively bind" mean that a construct or binding domain of the present invention does not bind to a protein or antigen other than said CD3, when said protein or antigen is expressed on the surface of a cell. The construct hence shows reactivity of $\leq 30\%$, preferably $\leq 20\%$, more preferably $\leq 10\%$, particularly preferably $\leq 9\%$, $\leq 8\%$, $\leq 7\%$, $\leq 6\%$, $\leq 5\%$, $\leq 4\%$, $\leq 3\%$, $\leq 2\%$, or $\leq 1\%$ with proteins or antigens other than CD3 (when said proteins or antigens are expressed on the surface of a cell), whereby binding to CD3, respectively, is set to be 100%. The "reactivity" can e.g. be expressed in an affinity value (see above).

[53] It is envisaged that the construct of the invention (and more specifically the domain comprising a paratope/binding domain that binds to human CD3epsilon) does not bind or does not significantly bind to CD3epsilon paralogues, more specifically to human CD3epsilon paralogues and/or to macaque / cyno CD3epsilon paralogues. It is also envisaged that the construct does not bind or does not significantly bind to (human or macaque / cyno) CD3epsilon paralogues on the surface of a target cell.

[54] The VH region as part of the binding domain binding to an extracellular epitope of the human CD3epsilon chain comprises a CDR-H1, a CDR-H2 and CDR-H3 sequence as set out herein above. The CDR sequences contain placeholders denoted as "X" for a given amino acid residue that can take the place of the placeholder as is common practice in the art. The placeholders are consecutively numbered in the format X_1 , X_2 , X_3 , and so forth, per given CDR sequence. The amino acid residues that can take place of the placeholder in the recited CDR sequences are listed according to preference, wherein the first listed amino acid is the most preferred, the second listed is the second most preferred, and so forth, if not otherwise specified, e.g. in other embodiments. If a sequence contains more than one placeholder, the same applies in relation to the preference of the amino acids; namely, it is the combination of the first listed amino acid residue for each of the placeholders that is most preferred, the combination of the second listed amino acid residue for each of the placeholders that is second most preferred, and so forth. This hierarchy of preference does not exclude the combination of amino acid residues for each of the placeholders independent of said preference hierarchy so that amino acid residues of different preference are combined. The same hierarchy is true for all amino acid residues that are listed herein below to take the place of a place holder in an amino acid sequence described herein below. Accordingly, the

above also applies for the placeholders denoted as "X" in the sequences of the VH and VL sequences and any other sequences recited throughout the specification.

[55] The CDR-H1 sequence comprises the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, T, or I; and X_2 is M or I. Following the above-explained hierarchy as regards the placeholder amino acids, the amino acids for the placeholders X_1 and X_2 are listed according to their preference, wherein the first listed amino acid is the most preferred, the second listed is the second-most preferred, and so forth. For X_1 , the amino acid K is most preferred, and for X_2 , the amino acid M is most preferred. A preferred combination is M for X_2 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_1 and X_2 , respectively. Preferred examples of the CDR-H1 sequence are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is most preferred.

[56] The CDR-H2 sequence comprises the amino acid sequence of RIRSKYNNYATYYADX₁VK X₂, where X_1 is S or Q; and X_2 is D, G, K, S, or E. For X_1 , the amino acid S is most preferred, and for X_2 , the amino acid D is most preferred. A preferred combination is S for X_1 in combination with any of the amino acid residues of X_2 , such as the combinations for X_1 and X_2 , respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of the CDR-H2 sequence are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred.

[57] The CDR-H3 sequence comprises the amino acid sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid I is most preferred; for X_3 , the amino acid Y is most preferred; and for X_4 , the amino acid W is most preferred. Preferred examples of the CDR-H3 sequence are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[58] The CDR-L1 sequence comprises the amino acid sequence of $X_1SSTGAVTX_2X_3X_4YX_5N$, where X_1 is G, R, or A; X_2 is S or T; X_3 is G or S; X_4 is N or Y; and X_5 is P or A. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid S is most preferred; for X_3 , the amino acid G is most preferred; for X_4 , the amino acid N is most preferred; and for X_5 , the amino acid P is most preferred. Preferred examples of the CDR-L1

sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred.

[59] The CDR-L2 sequence comprises the amino acid sequence of $X_1TX_2X_3X_4X_5X_6$; where
 5 X_1 is G or A; X_2 is K, D, or N; X_3 is F, M or K; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid K is most preferred; for X_3 , the amino acid F is most preferred; for X_4 , the amino acid L is most preferred; for X_5 , the amino acid A is most preferred and for X_6 , the amino acid P is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and
 10 GTNKRAP, wherein GTKFLAP is most preferred.

[60] The CDR-L3 sequence comprises the amino acid sequence of $X_1LWYSNX_2WV$, where X_1 is V, A, or T; and X_2 is R or L. For X_1 , the amino acid V is most preferred, and for X_2 , the amino acid R is most preferred. Preferred combinations are R for X_2 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 ,
 15 respectively, selected from V and R, A and R, T and R, most preferred the combination V and R. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, TLWYSNRWV, and ALWYSNLWV, wherein VLWYSNRWV is most preferred.

[61] In a preferred embodiment, said VH region of i) comprises: a CDR-H1 sequence comprising or consisting of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, or I; and X_2 is M or I; a CDR-H2 sequence of RIRSKYNNYATYYADX₁VKX₂, where X_1 is S or Q; and X_2 is D, G, K, S, or E; and a CDR-H3 sequence of HX₁NFGNSYX₂SX₃X₄AY, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and said VL region of ii) comprises: a CDR-L1 sequence of $X_1SSTGAVTSGX_2YPN$, where X_1 is G, R, or A; and X_2
 25 is N or Y; a CDR-L2 sequence of $X_1TX_2X_3X_4X_5X_6$; where X_1 is G or A; X_2 is K or D; X_3 is F or M; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S; and a CDR-L3 sequence of $X_1LWYSNRWV$, where X_1 is V, A, or T; and wherein said one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from X_24V or X_24F in CDR-H1; D15 (preferably E), X_116A in CDR-H2; H1 (preferably A or N),
 30 X_12E , F4 (preferably I), and/or N6 (preferably S or T) in CDR-H3; and W93 (preferably Y) in CDR-L3.

[62] Said CDR-H1 sequence comprises or consists of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, or I; and X_2 is M or I. For X_1 , the amino acid K is most preferred, and for X_2 , the amino acid M is most preferred. A preferred combination is M for X_2
 35 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_1 and X_2 , respectively.

Preferred examples of the CDR-H1 sequence are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is preferred, wherein KYAMN is most preferred.

[63] Said CDR-H2 sequence comprises or consist of the amino acid sequence of
 5 RIRSKYNNYATYYADX₁VK X₂, where X₁ is S or Q; and X₂ is D, G, K, S, or E. For X₁, the amino acid S is most preferred, and for X₂, the amino acid D is most preferred. A preferred combination is S for X₁ in combination with any of the amino acid residues of X₂, such as the combinations for X₁ and X₂, respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of the CDR-H2 sequence are
 10 selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred.

[64] The CDR-H3 sequence comprises the amino acid sequence of
 15 HX₁NFGNSYX₂SX₃X₄AY, where X₁ is G, R, or A; X₂ is I, L, V, or T; X₃ is Y, W or F; and X₄ is W, F or Y. For X₁, the amino acid G is most preferred; for X₂, the amino acid I is most preferred; for X₃, the amino acid Y is most preferred; and for X₄, the amino acid W is most preferred. Preferred examples of the CDR-H3 sequence are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY,
 20 HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[65] The CDR-L1 sequence comprises the amino acid sequence of
 X₁SSTGAVTSGX₂YPN, where X₁ is G, R, or A; and X₂ is N or Y. For X₁, the amino acid G is most preferred; and for X₂, the amino acid N is preferred. Preferred examples of the CDR-L1
 25 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, and ASSTGAVTSGNYPN, wherein GSSTGAVTSGNYPN or ASSTGAVTSGNYPN is preferred, wherein GSSTGAVTSGNYPN is most preferred.

[66] The CDR-L2 sequence comprises the amino acid sequence of X₁TX₂X₃X₄X₅X₆; where
 30 X₁ is G or A; X₂ is K or D; X₃ is F or M; X₄ is L or R; X₅ is A, P, or V; and X₆ is P or S. For X₁, the amino acid G is most preferred; for X₂, the amino acid K is most preferred; for X₃, the amino acid F is most preferred; for X₄, the amino acid L is most preferred; for X₅, the amino acid A is most preferred and for X₆, the amino acid P is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, and GTKFLVP, wherein GTKFLAP or GTKFLVP is preferred, wherein GTKFLAP is most preferred.

[67] The CDR-L3 sequence comprises the amino acid sequence of X₁LWYSNRWW,
 35 where X₁ is V, A, or T, wherein the amino acid V is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, and TLWYSNRWW,

wherein VLWYSNRWV or TLWYSNRWV is more preferred, wherein VLWYSNRWV is most preferred.

[68] In a further preferred embodiment, said VH region of i) comprises: a CDR-H1 sequence comprising or consisting of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, R, or I; and X_2 is M or I; a CDR-H2 sequence of RIRSKYNNYATYYAD X_1VKX_2 , where X_1 is S or Q; and X_2 is D, G, K, or S; and a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and said VL region of ii) comprises: a CDR-L1 sequence of $X_1SSTGAVTSGX_2YPN$, where X_1 is G or A; and X_2 is N or Y; a CDR-L2 sequence of $GTKFLX_1P$; where X_1 is A or V; and a CDR-L3 sequence of $X_1LWYSNRWV$, where X_1 is V, A, or T; and wherein said one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from X_24V or X_24F in CDR-H1; D15 (preferably E), X_116A in CDR-H2; H1 (preferably A or N), X_12E , F4 (preferably I), and/or N6 (preferably S or T) in CDR-H3; and W93 (preferably Y) in CDR-L3.

[69] Said CDR-H1 sequence comprises or consists of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, R, or I; and X_2 is M or I. For X_1 , the amino acid K is most preferred, and for X_2 , the amino acid M is most preferred. A preferred combination is M for X_2 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_1 and X_2 , respectively. Preferred examples of the CDR-H1 sequence are selected from KYAMN, VYAMN, SYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is preferred, wherein KYAMN is most preferred.

[70] Said CDR-H2 sequence comprises or consist of the amino acid sequence of RIRSKYNNYATYYAD X_1VKX_2 , where X_1 is S or Q; and X_2 is D, G, K, or S. For X_1 , the amino acid S is most preferred, and for X_2 , the amino acid D is most preferred. A preferred combination is S for X_1 in combination with any of the amino acid residues of X_2 , such as the combinations for X_1 and X_2 , respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of the CDR-H2 sequence are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD is preferred, wherein RIRSKYNNYATYYADSVKD is most preferred.

[71] Said CDR-H3 sequence comprises or consist of the amino acid sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid I is most preferred; for X_3 , the amino acid Y is most preferred; and for X_4 , the amino acid W is most preferred.

Preferred examples of the CDR-H3 sequence are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, and HANFGNSYISYWAY, wherein HGNFGNSYISYWAY or HANFGNSYISYWAY is preferred, wherein HGNFGNSYISYWAY is most preferred.

[72] Said CDR-L1 sequence comprises or consists the amino acid sequence of X_1 SSTGAVTSG X_2 YPN, where X_1 is G or A; and X_2 is N or Y. For X_1 , the amino acid G is most preferred; and for X_2 , the amino acid N is preferred. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, GSSTGAVTSGYYPN, and ASSTGAVTSGNYPN, wherein GSSTGAVTSGNYPN or ASSTGAVTSGNYPN is preferred, wherein GSSTGAVTSGNYPN is most preferred.

[73] Said CDR-L2 sequence comprises or consists of the amino acid sequence of GTKFL X_1 P; where X_1 is A or V. For X_1 , the amino acid A is preferred. Said CDR-L2 sequence is GTKFLAP or GTKFLVP, wherein GTKFLAP is preferred.

[74] The CDR-L3 sequence comprises or consists of the amino acid sequence of X_1 LWYSNRWV, where X_1 is V, A, or T, wherein the amino acid V is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, and TLWYSNRWV, wherein VLWYSNRWV or TLWYSNRWV is more preferred, wherein VLWYSNRWV is most preferred.

[75] In an even more preferred embodiment, said VH region of i) comprises: a CDR-H1 sequence comprising or consisting of the amino acid sequence of X_1 YAMN, where X_1 is K or S; a CDR-H2 sequence of RIRSKYNNYATYYADSVK X_1 , where X_1 is D or G; and a CDR-H3 sequence of HGNFGNSY X_1 S X_2 WAY, where X_1 is I or V; and X_2 is Y or W; and said VL region of ii) comprises: a CDR-L1 sequence of GSSTGAVTSG X_1 YPN, where X_1 is N or Y; a CDR-L2 sequence of GTKFLAP; and a CDR-L3 sequence of X_1 LWYSNRWV, where X_1 is V or A; and wherein said one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from M4V or M4F in CDR-H1; D15 (preferably E), S16A in CDR-H2; H1 (preferably A or N), G2E, F4 (preferably I), and/or N6 (preferably S or T) in CDR-H3; and W93 (preferably Y) in CDR-L3.

[76] Said CDR-H1 sequence comprises or consists of the amino acid sequence of X_1 YAMN, where X_1 is K or S, wherein the amino acid K is preferred. Said CDR-H1 sequence is KYAMN or SYAMN, wherein KYAMN is most preferred.

[77] Said CDR-H2 sequence comprises or consist of the amino acid sequence of RIRSKYNNYATYYADSVK X_1 , where X_1 is D or G. For X_1 , the amino acid D is preferred. Said CDR-H2 sequence is RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADSVKG, wherein RIRSKYNNYATYYADSVKD is preferred.

[78] Said CDR-H3 sequence comprises or consist of the amino acid sequence of HGNFGNSYX₁SX₂WAY, where X₁ is I or V; and X₂ is Y or W. For X₁, the amino acid I is preferred; for X₂, the amino acid Y is preferred. Said CDR-H3 sequence is HGNFGNSYISYWAY or HGNFGNSYVSWWAY, wherein HGNFGNSYISYWAY is preferred.

5 [79] Said CDR-L1 sequence comprises or consists the amino acid sequence of GSSTGAVTSGX₁YPN, where X₁ is N or Y. For X₁, the amino acid N is preferred. Said CDR-L1 sequence is GSSTGAVTSGNYPN or GSSTGAVTSGYYPN, wherein GSSTGAVTSGNYPN is preferred.

10 [80] Said CDR-L2 sequence comprises or consists of the amino acid sequence of GTKFLAP.

[81] The CDR-L3 sequence comprises or consists of the amino acid sequence of X₁LWYSNRWV, where X₁ is V or A, wherein V is preferred. Said CDR-L3 sequence VLWYSNRWV or ALWYSNRWV, wherein VLWYSNRWV is preferred.

15 [82] Each of the CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 sequences be freely combined in the format CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3 (this is the preferred orientation of the VH and the VL region) or CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, CDR-H3 and exhibiting the recited binding to an extracellular epitope of the human CD3ε chain.

20 [83] Preferred combinations of CDR-L1 to L3 sequences of the VL region and preferred combinations of CDR-H1 to H3 sequences of the VH region are listed in the below Table 1.

CDR-L1	CDR-L2	CDR-L3
GSSTGAVTSGYYPN	GTKFLAP	ALWYSNRWV
RSSTGAVTSGYYPN	ATDMRPS	ALWYSNRWV
GSSTGAVTSGNYPN	GTKFLAP	VLWYSNRWV
ASSTGAVTSGNYPN	GTKFLVP	TLWYSNRWV
RSSTGAVTTSNYAN	GTNKRAP	ALWYSNLWV
CDR-H1	CDR-H2	CDR-H3
IYAMN	RIRSKYNNYATYYADSVKS	HGNFGNSYVSFFAY
KYAMN	RIRSKYNNYATYYADSVKD	HGNFGNSYISYWAY

SYAMN	RIRSKYNNYATYYADSVKG	HGNFGNSYLSFWAY
RYAMN	RIRSKYNNYATYYADSVKG	HGNFGNSYLSYFAY
VYAMN	RIRSKYNNYATYYADSVKK	HGNFGNSYLSWWAY
KYAMN	RIRSKYNNYATYYADSVKS	HGNFGNSYTSYYAY
GYAMN	RIRSKYNNYATYYADSVKE	HRNFGNSYLSWFAY
VYAMN	RIRSKYNNYATYYADSVKK	HGNFGNSYISWWAY
SYAMN	RIRSKYNNYATYYADSVKG	HGNFGNSYVSWWAY
KYAIN	RIRSKYNNYATYYADQVKD	HANFGNSYISYWAY
TYAMN	RIRSKYNNYATYYADSVKD	HGNFGNSYVSWFAY

Table 1

- [84]** Preferably, any of the above listed combinations of CDR-L1 to L3 combinations is combined with any of the above-listed combinations CDR-H1 to H3 as part of the binding domain binding to an extracellular of the human CD3 ϵ chain. In other words, the VL region comprises or consists of as CDR-L1, CDR-L2, CDR-L3 sequence, in this order,
- GSSTGAVTSGYYPN, GTKFLAP, ALWYSNRWV;
 RSSTGAVTSGYYPN, ATDMRPS, ALWYSNRWV;
- GSSTGAVTSGNYPN, GTKFLAP, VLWYSNRWV;
 ASSTGAVTSGNYPN, GTKFLVP, TLWYSNRWV; or
 RSSTGAVTTSNYAN, GTNKRAP, ALWYSNLWV; and
 the VL region comprises or consists of as CDR-H1, CDR-H2, CDR-H3 sequence, in this order,
- IYAMN, RIRSKYNNYATYYADSVKS, HGNFGNSYVSFFAY;
 KYAMN, RIRSKYNNYATYYADSVKD, HGNFGNSYISYWAY;
 SYAMN, RIRSKYNNYATYYADSVKG, HGNFGNSYLSFWAY;
 RYAMN, RIRSKYNNYATYYADSVKG, HGNFGNSYLSYFAY;
 VYAMN, RIRSKYNNYATYYADSVKK, HGNFGNSYLSWWAY;
- KYAMN, RIRSKYNNYATYYADSVKS, HGNFGNSYTSYYAY;
 GYAMN, RIRSKYNNYATYYADSVKE, HRNFGNSYLSWFAY;
 VYAMN, RIRSKYNNYATYYADSVKK, HGNFGNSYISWWAY;
 SYAMN, RIRSKYNNYATYYADSVKG, HGNFGNSYVSWWAY;
 KYAIN, RIRSKYNNYATYYADQVKD, HANFGNSYISYWAY; or
 TYAMN, RIRSKYNNYATYYADSVKD, HGNFGNSYVSWFAY.

In accordance with the invention, preferred CDR sequence combinations of the VH and the

VL regions, listed in the order CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3, are as defined in SEQ ID NOs: 118 to 123, 166 to 171, 356 to 361, 546 to 551, 724 to 729, 922 to 927, 1100 to 1105, 1290 to 1295, 1468 to 1473, 1658 to 1663, 1848 to 1853.

- 5 Most preferred is that the VL region comprises as CDR-L1, CDR-L2, CDR-L3 sequence, listed in this order,
GSSTGAVTSGNYPN, GTKFLAP, VLWYSNRWV; and
the VL region comprises as CDR-H1, CDR-H2, CDR-H3 sequence, listed in this order,
KYAMN, RIRSKYNNYATYYADSVKD, HGNFGNSYISYWAY; as depicted in SEQ ID NOs:
10 1848 to 1853. Preferably the orientation of the CDRs is VH to VL, i.e. the orientation of the variable regions is from N- to C-terminus VH to VL.

[85] In accordance with the invention, said CDR sequences of the VH and/or the VL region comprise one or more amino acid substitutions. As is common in the art, the position and nature of amino acid substitutions are denoted herein by indicating the original amino acid residue at the position to be substituted and the amino acid used for substitution in the format of, e.g., F4I, wherein "F" denotes the original amino acid residue occurring at position "4" of the given amino acid sequence and "I" denotes the amino acid residue which substituted "F" at position 4. In case substitution is by any amino acid residue (other than the original amino acid residue), no amino acid residue is indicated, but only the originally occurring amino acid residue and its position in the given amino acid sequence, so that the previous example would be denoted as "F4" only. Preferably, only naturally occurring amino acids are used for substitution.

[86] The VH region of i) and/or VL region of ii) comprise one or more amino acid substitutions as specified herein in one or more CDR sequences as recited herein above. Accordingly, at least one of the recited amino acid substitutions of the variable regions is comprised in said binding domain binding to an extracellular epitope of the human CD3ε chain. Said at least one or one or more amino acid substitution, in the case that only one amino acid substitution is present, can be present in a CDR sequence in said VH or said VL region or, in case more than one amino acid substitution is present, in CDRs in both the VH and the VL region or restricted to CDR sequences in only the VH or the VL region. In certain embodiments where there are more than one amino acid substitutions, the substitutions are in the VH and the VL region or, alternatively, only in one variable region. Preferably, the substitutions are in the CDRs of the VH and the VL region.

[87] In case the CDR-H1 is to comprise an amino acid substitution at position 4 it is, preferably, the substitution of the original amino acid with the amino acid V. Preferably, the CDR-H1 sequence is KYAIN or KYAMN, i.e. comprising none of said recited amino acid

substitutions.

[88] In CDR-H2, the amino acid substitution at position 15 is, preferably, D15E, or the amino acid substitution at position 16 with amino acid A. Preferably, CDR-H1 comprises the amino acid residue substitution at position 16 with amino acid A; in this case, a preferred amino acid for the last amino acid of CDR-H2 is D or G, most preferred D. Hence, a preferred CDR-H2 sequence is RIRSKYNNYATYYADAVKD or RIRSKYNNYATYYADAVKG, with RIRSKYNNYATYYADAVKD more preferred. In case CDR-H2 contains two amino acid substitutions, the combination of the amino acid E at position 15 and amino acid A at position 16 are preferred; in this case, a preferred amino acid for the last amino acid of CDR-H2 is G. Hence, a preferred CDR-H2 sequence for the combination of the amino acid E at position 15 and amino acid A at position 16 is RIRSKYNNYATYYAEAVKG.

[89] In CDR-H3, the amino acid substitutions are at position 1, preferably a substitution with amino acid A or N, at position 2 with amino acid E, at position 4, preferably with amino acid I, and at position 6, preferably with amino acid S or T. Preferably, CDR-H3 comprises the amino acid A or N at position 1, the amino acid S or T at position 6; in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, preferred amino acids for X_1 are G or A, most preferred G; for X_2 is I; for X_3 is Y; and for X_4 are W or Y. In case CDR-H3 comprises two amino acid substitutions, preferred combinations are the amino acid A at position 1 and the amino acid S at position 6; and the amino acid N at position 1 and the amino acid T at position 6; in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_1 is G or A, most preferred G; for X_2 is I, for X_3 is Y, and for X_4 are W and F. In case CDR-H3 comprises three amino acid substitutions, preferred combinations are the amino acid A at position 1, the amino acid I at position 4, and the amino acid S at position 6; and the amino acid N at position 1, the amino acid I at position 4 and the amino acid T at position 6, in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_2 is I, for X_3 is Y, and for X_4 are W and F. In case CDR-H3 comprises four amino acid substitutions, a preferred combination is the amino acid N at position 1, the amino acid E at position 2, the amino acid I at position 4, and the amino acid T at position 6; in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_2 is I, for X_3 is Y, and for X_4 is W. Hence, preferred CDR-H3 sequences are selected from AGNFGSSYISYWAY, NENIGTSYISYWAY, AGNFGTSYISYWAY, NANFGTSYISYFAY, and AGNFGSSYISYFAY, with AGNFGSSYISYWAY and AGNFGSSYISYFAY most preferred.

[90] In CDR-L3, the amino acid substitution at position 1 is with amino acid L or the amino acid substitution is W93, preferably W93Y (which may also be referred to as X_1 93Y), in the sequence of X_1 LWYSN X_2 WV, where X_1 is V, A, or T; and X_2 is R or L. Preferably, the CDR-

L3 sequence is VLYYSNRWW when CDR-L3 comprises only one amino acid substitution. It is preferred, however, that CDR-L3 does not comprise said X₁L and W93 amino acid substitution, in which case a preferred CDR-L3 sequence is VLYYSNRWW.

[91] Without wishing to be bound by a specific scientific theory, each of the above recited amino acid substitution(s) lead(s) to an increase in thermal stability of the binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region linked to a VL region as described herein as compared to the binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region linked to a VL region sequence that is unmodified, i.e. does not contain said amino acid residue substitution(s). Said increase of the temperature stability is, preferably, measured by the well know and also herein described method of Differential Scanning Fluorimetry (DSF). Said method is, e.g., described in Wen et al., "Nano differential scanning fluorimetry for comparability studies of therapeutic proteins", Analytical Biochemistry, Volume 593, 2020, 113581, ISSN 0003-2697; or Dart, M. L., et al. (2018). "Homogeneous Assay for Target Engagement Utilizing Bioluminescent Thermal Shift". ACS medicinal chemistry letters, 9(6), 546–551). As evident from the example section, it was shown that the amino acid substitutions or combinations thereof as defined herein result in an increased thermal stability (see Example 1, Table 2 and 3) as compared to the unmodified CD3 binding domain defined herein ("I2C") while the cytotoxic activity was maintained which was not the case with a prior art method to improve thermal stability, namely the CC44/100 cys clamp, in which an additional disulfide bond was engineered for stabilizing (Reiter, Y. et al., 1994) by replacing the amino acid residues with cysteine residues at position 44 in the heavy chain variable region and at position 100 in the light chain variable region (numbering scheme according to Kabat et al., 1991) of the unmodified CD3 binding domain defined herein (VH and VL SEQ ID NOs: 1854 and 1855, respectively; see Example 2, Table 5). The VH and VL region combinations of the CD3ε binding domain described herein are therefore temperature stabilized as compared to the VH and VL region sequence that does not contain the given substitution(s) that are introduced at the positions defined herein.

[92] In a preferred embodiment of the polypeptide or polypeptide construct of claim 1 of the invention, in addition to said one amino acid substitution or a combination thereof as defined in iii) X₂ is I in said CDR-H1 sequence; X₂ is G in said CDR-H2 sequence; X₁ is A, X₄ is F in said CDR-H3 sequence; and/or X₁ is A in said CDR-L3 sequence. The one amino acid substitution or combination thereof as defined herein is/are in addition combined with specific amino acids at specific positions in the CDRs. Hence, at least one of the recited amino acid substitutions in accordance with iii) is present and at least one of X₂ is G in said CDR-H2 sequence; X₁ is A, X₄ is F in said CDR-H3; and/or X₁ is A in said CDR-L3 sequence is additionally present in the CDRs. As previously stated herein above, a preferred amino acid

for X_2 is I in said CDR-H1 sequence or X_2 is G in said CDR-H2 sequence, if only one additional amino acid is present in the CDRs, wherein it is most preferred that X_2 is I in said CDR-H1 sequence. A preferred combination of two of said additional amino acids is X_2 is I in said CDR-H1 sequence and X_4 is F in said CDR-H3 sequence; or X_2 is G in said CDR-H2 sequence and X_4 is F in said CDR-H3 sequence. A preferred combination of three of said additional amino acids is X_2 is I in said CDR-H1 sequence, X_1 is A, and X_4 is F in said CDR-H3 sequence; or X_2 is I in said CDR-H1 sequence, X_4 is F in said CDR-H3 sequence, and X_1 is A in said CDR-L3 sequence. Since the latter amino acids are to be present additionally, it is understood that those recited additional amino acids that overlap in position with the amino acid substitution of iii) cannot replace the overlapping amino acid substitution. For example, if the only amino acid substitution in accordance with iii) is either X_2 4V or X_2 4F in CDR-H1, said amino acid cannot be replaced by amino acid I in said CDR-H1 sequence, since there would be no amino acid substitution as defined in iii) remaining in the binding domain. In other terms, there must always be at least one of the amino acid substitutions as defined in iii) comprised in the polypeptide or polypeptide construct of the invention.

[93] It is also understood that depending on the actual sequence of the CDRs, one or more of said additional amino acids may already be part of the CDRs as defined herein above or, if this is not the case, those CDRs will be changed to exhibit said additional amino acid(s) in combination with one amino acid substitution or a combination thereof as recited in iii).

[94] In another preferred embodiment, the polypeptide or polypeptide construct of the invention comprises or consists of combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more amino acid substitutions, or of up to two, three, four, five, six, seven, eight, nine, ten, eleven, twelve amino acid substitutions. Preferably, only the substitution(s) defined herein are introduced in the VH and the VL region sequence. This applies to all embodiments recited herein so that the VH and the VL region sequence consists of the unmodified amino acid sequence with the substitution(s) as defined herein.

[95] More specifically, it is preferred that i) said one amino acid substitution is selected from: a. X_2 4V or X_2 4F in CDR-H1; H1A in CDR-H3; and b. X_1 1L and W3Y in CDR-L3; ii) said combination of two or more amino acid substitutions are selected from X_1 16A in CDR-H2 and N6S in CDR-H3; and X_1 16A in CDR-H2 and N6T in CDR-H3; iii) said combination of three or more amino acid substitutions are selected from X_1 16A in CDR-H2, H1A and N6S in CDR-H3; X_1 16A in CDR-H2, H1A and N6T in CDR-H3; X_1 16A in CDR-H2, H1N and N6T in CDR-H3; iv) said combination of four or more amino acid substitutions are selected from X_1 16A in CDR-H2, H1A, N6S in CDR-H3, and W3Y in CDR-L3; D15E, X_1 16A in CDR-H2, H1A, and N6T in CDR-H3; D15E, X_1 16A in CDR-H2, H1A, and N6S in CDR-H3; X_1 16A in CDR-H2,

H1A, F4I and N6S in CDR-H3; v) said combination of five or six amino acid substitutions are selected from X₁16A in CDR-H2, H1A, X₁2E, F4I, and N6T in CDR-H3; X₁16A in CDR-H2, H1N, X₁2E, F4I, and N6S in CDR-H3; D15E, X₁16A in CDR-H2, H1A, N6S in CDR-H3; and W3Y in CDR-L3; D15E, X₁16A in CDR-H2, H1N, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, H1A, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, X₁2E, F4I and N6T in CDR-H3.

[96] In accordance with the foregoing, the amino acid substitution H1A in CDR-H3 is preferably the amino acid substitution, in case there is only one amino acid substitution in the CD3epsilon binding domain, within the CDR sequences or the VH region sequences as defined herein. Furthermore, in case of combinations of amino acid substitutions as defined in iii) preferably H1A in CDR-H3 is one of the amino acid substitutions of said combination.

[97] In an embodiment, the invention relates to a polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region,, wherein

i) the VH region comprises the sequence of EVX₁LX₂ESGGGLX₃QPX₄GSLKLSCAASGFTFNX₅YAX₆NWVRQAPGKGLEWVA RIRSKYNNYATYYADX₇VKX₈RFTISRDDX₉X₁₀X₁₁X₁₂YLQMNNLKTEDTAX₁₃YYC VRHX₁₄NFGNSYX₁₅SX₁₆X₁₇AYWGQGTLVTVSX₁₈, where X₁ is Q or K; X₂ is V or L; X₃ is V or E; X₄ is G or K; X₅ is K, V, S, G, R, T, or I; X₆ is M or I; X₇ is S or Q; X₈ is D, G, K, S, or E; X₉ is K or Q; X₁₀ is N or S; X₁₁ is T or I; X₁₂ is A or L; X₁₃ is V or M; X₁₄ is G, R or A; X₁₅ is I, L, V, or T; X₁₆ is Y, W or F; X₁₇ is W, F or Y; and X₁₈ is S or A; and

ii) the VL region comprises the sequence of QX₁VVTQEX₂X₃LTX₄SPGX₅TVTLTCX₆SSTGAVTX₇X₈X₉YX₁₀NWVQX₁₁KPX₁₂X₁₃ X₁₄X₁₅X₁₆GLIGX₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂GX₂₃PARFSGSLX₂₄GX₂₅KAALTX₂₆X₂₇GX₂₈QX₂₉EDEAX₃₀YX₃₁CX₃₂LWYSNX₃₃WVFGGGTKLTVL, where X₁ is T or A; X₂ is P or S; X₃ is S or A; X₄ is V or T; X₅ is G or E; X₆ is G, R, or A; X₇ is S or T; X₈ is G or S; X₉ is N or Y; X₁₀ is P or A; X₁₁ is Q or E; X₁₂ is G or D; X₁₃ is Q or H; X₁₄ is A or L; X₁₅ is P or F; X₁₆ is R or T; X₁₇ is G or A; X₁₈ is K or D; X₁₉ is F or M; X₂₀ is L or R; X₂₁ is A, P or V; X₂₂ is P or S; X₂₃ is T or V; X₂₄ is L or I; X₂₅ is G or D; X₂₆ is L or I; X₂₇ is S or T; X₂₈ is V or A; X₂₉ is P or T; X₃₀ is E or I; X₃₁ is Y or F; X₃₂ is V, A, or T; X₃₃ is R or L; and

iii) wherein the VH and/or VL region sequence comprises one or more amino acid substitutions selected from

a. N30 (preferably S), X₆34V, X₆34F, Q39 (E, K, R, D, preferably E), L45 (M or V, preferably M), D64 (preferably E), X₇65A, X₁₂81V, X₁₂81T, X₁₂81I, V99 (A or L,

preferably A), H101 (preferably A or N), X₁₄102E, F104 (preferably I), and N106 (preferably S or T) in the VH region sequence in i); and

- b. L20 (preferably I or M), V38 (preferably I), X₁₁40R, X₁₁40K, X₂₄69 (S or E, preferably S), X₃₂91L, X₃₃93 (preferably Y), and G102 (preferably S) in the VL region sequence in ii).

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[98] In this embodiment, preferred VH and VL region sequences comprised in the binding domain and mediating the binding to the human CD3ε chain are described. As evident from the above, the VH and VL region sequences of i) and ii) comprise various placeholders, wherein the same hierarchy and nomenclature applies for the placeholders as recited herein above in the context of the CDRs comprised in said VH and VL region of i) and ii). As is evident from the sequences for the VH and VL region, said CDRs described herein above are part of said VH and VL region sequence. Accordingly, the preferred embodiments of said CDRs of i) and ii) as described herein above also apply to this preferred embodiment.

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[99] The VH region of i) comprises or consists of the sequence of EVX₁LX₂ESGGGLX₃QPX₄GSLKLSCAASGFTFNX₅YAX₆NWVRQAPGKGLEWWARIRSKYNNYATYYADX₇VKX₈RFTISRDDSX₉X₁₀X₁₁X₁₂Y LQMNNLKTEDTAX₁₃YYCVRHX₁₄NFGNSYX₁₅SX₁₆X₁₇AYWGQGT LTVSX₁₈, where X₁ is Q or K; X₂ is V or L; X₃ is V or E; X₄ is G or K; X₅ is K, V, S, G, R, T, or I; X₆ is M or I; X₇ is S or Q; X₈ is D, G, K, S, or E; X₉ is K or Q; X₁₀ is N or S; X₁₁ is T or I; X₁₂ is A or L; X₁₃ is V or M; X₁₄ is G, R or A; X₁₅ is I, L, V, or T; X₁₆ is Y, W or F; X₁₇ is W, F or Y; and X₁₈ is S or A.

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[100] The CDR sequences within said VH region are as follows: a CDR-H1 sequence comprising or consisting of X₅YAX₆N; a CDR-H2 sequence comprising or consisting of RIRSKYNNYATYYADX₇VKX₈; and a CDR-H3 sequence comprising or consisting of HX₁₄NFGNSYX₁₅SX₁₆X₁₇AY. Preferred examples of said CDR-H1 sequence X₅YAX₆N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is most preferred. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₇VKX₈ are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred. Preferred examples of said CDR-H3 sequence HX₁₄NFGNSYX₁₅SX₁₆X₁₇AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

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[101] For X₁, the amino acid Q is preferred. For X₂, the amino acid V is preferred. For X₃,

the amino acid V is preferred. For X₄, the amino acid G is preferred. For X₅, the amino acid K is most preferred, and for X₆, the amino acid M is most preferred. A preferred combination for X₅ and X₆ is M for X₆ in combination with any of the amino acid residues of X₅, such as the combinations for X₅ and X₆, respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X₅ and X₆, respectively. Preferred examples of said CDR-H1 sequence X₅YAX₆N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is most preferred. For X₇, the amino acid S is most preferred, and for X₈, the amino acid D is most preferred. A preferred combination is S for X₇ in combination with any of the amino acid residues of X₈, such as the combinations for X₇ and X₈, respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₇VKX₈ are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred. For X₉, the amino acid K is preferred. For X₁₀, the amino acid N is preferred. For X₁₁, the amino acid T is preferred. For X₁₂, the amino acid A is preferred. For X₁₃, the amino acid V is preferred. For X₁₄, the amino acid G is most preferred; for X₁₅, the amino acid I is most preferred; for X₁₆, the amino acid Y is most preferred; and for X₁₇, the amino acid W is most preferred. Preferred examples of said CDR-H3 sequence HX₁₄NFGNSYX₁₅SX₁₆X₁₇AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred. For X₁₈, the amino acid sequence S is preferred.

[102] The VL region of ii) comprises or consists of the sequence of QX₁VVTQEX₂X₃LTX₄SPGX₅TVTLTCX₆SSTGAVTX₇X₈X₉YX₁₀NWVQX₁₁KPX₁₂X₁₃X₁₄X₁₅X₁₆GLIGX₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂GX₂₃PARFSGSLX₂₄GX₂₅KAALTX₂₆X₂₇GX₂₈QX₂₉EDEAX₃₀YX₃₁CX₃₂LWYSNX₃₃WFGGGTKLTVL, where X₁ is T or A; X₂ is P or S; X₃ is S or A; X₄ is V or T; X₅ is G or E; X₆ is G, R, or A; X₇ is S or T; X₈ is G or S; X₉ is N or Y; X₁₀ is P or A; X₁₁ is Q or E; X₁₂ is G or D; X₁₃ is Q or H; X₁₄ is A or L; X₁₅ is P or F; X₁₆ is R or T; X₁₇ is G or A; X₁₈ is K or D; X₁₉ is F or M; X₂₀ is L or R; X₂₁ is A, P or V; X₂₂ is P or S; X₂₃ is T or V; X₂₄ is L or I; X₂₅ is G or D; X₂₆ is L or I; X₂₇ is S or T; X₂₈ is V or A; X₂₉ is P or T; X₃₀ is E or I; X₃₁ is Y or F; X₃₂ is V, A, or T; and X₃₃ is R or L.

[103] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of X₆SSTGAVTX₇X₈X₉YX₁₀N; a CDR-L2 sequence comprising or consisting of X₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂; and a CDR-L3 sequence comprising or consisting of

X₃₂LWYSNX₃₃WV. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, TLWYSNRWV, and ALWYSNLWV, wherein VLWYSNRWV is most preferred.

[104] For X₁, the amino acid T is preferred. For X₂, the amino acid P is preferred. For X₃, the amino acid S is preferred. For X₄, the amino acid V is preferred. For X₅, the amino acid G is preferred. For X₆, the amino acid G is most preferred. For X₇, the amino acid S is most preferred. For X₈, the amino acid G is most preferred. For X₉, the amino acid N is most preferred. For X₁₀, the amino acid P is most preferred. X₆ to X₁₀ are part of the CDR-L1 sequence within the VL region. Preferred examples of said CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. For X₁₁, the amino acid Q is preferred. For X₁₂, the amino acid G is preferred. For X₁₃, the amino acid Q is preferred. For X₁₄, the amino acid A is preferred. For X₁₅, the amino acid P is preferred. For X₁₆, the amino acid R is preferred. For X₁₇, the amino acid G is preferred. For X₁₈, the amino acid K is preferred. For X₁₉, the amino acid F is preferred. For X₂₀, the amino acid L is preferred. For X₂₁, the amino acid A is preferred. For X₂₂, the amino acid P is preferred. X₁₇ to X₂₂ are part of the CDR-L2 sequence of the VL region. Preferred examples of said CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. For X₂₃, the amino acid T is preferred. For X₂₄, the amino acid L is preferred. For X₂₅, the amino acid G is preferred. For X₂₆, the amino acid L is preferred. For X₂₇, the amino acid S is preferred. For X₂₈, the amino acid V is preferred. For X₂₉, the amino acid P is preferred. For X₃₀, the amino acid E is preferred. For X₃₁, the amino acid Y is preferred. For X₃₂, the amino acid V is preferred. For X₃₃, the amino acid R is preferred. X₃₂ and X₃₃ are part of the CDR-L3 sequence of the VL region. Preferred examples of said CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, TLWYSNRWV, and ALWYSNLWV, wherein VLWYSNRWV is most preferred.

[105] In a more preferred embodiment, the VH region of i) comprises or consists of the sequence of EVQLVESGGGLX₁QPGGSLKLSKAASGFTFNX₂YAX₃NWVRQAPGKGLEWVARIRSKYNNYATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYWGQGTLLTVSS, where X₁ is V or E; X₂ is K, V, S, G, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G, K, S, or E; X₆ is G, R or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F; and the VL region of ii) comprises or consists of the sequence of

QTVVTQEPSLTVSPGGTVTLTCX₁SSTGAVTSGX₂YPNWWQQKPGQAPRGLIGX₃TX₄X₅X₆X₇X₈GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCX₉LWYSNRWWFGGGTKLTVL, where X₁ is G, R, or A; X₂ is N or Y; X₃ is G or A; X₄ is K or D; X₅ is F or M; X₆ is L or R; X₇ is A, P or V; X₈ is P or S; and X₉ is V, A, or T.

- 5 **[106]** The VH region of i) comprises or consists of the sequence of EVQLVESGGGLX₁QPGGSLKLSCAASGFTFNX₂YAX₃NWVRQAPGKGLEWWARIRSKYNNYATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYWGQGTLLTVSS, where X₁ is V or E; X₂ is K, V, S, G, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G, K, S, or E; X₆ is G, R or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F.
- 10 **[107]** The CDR sequences within said VH region are as follows: a CDR-H1 sequence comprising or consisting of X₂YAX₃N; a CDR-H2 sequence comprising or consisting of RIRSKYNNYATYYADX₄VKX₅; and a CDR-H3 sequence comprising or consisting of HX₆NFGNSYX₇SX₈X₉AY. Preferred examples of said CDR-H1 sequence X₂YAX₃N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN,
- 15 wherein KYAMN or KYAIN is more preferred, wherein KYAMN is most preferred. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₄VKX₅ are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD is more preferred,
- 20 wherein RIRSKYNNYATYYADSVKD is most preferred. Preferred examples of said CDR-H3 sequence HX₆NFGNSYX₇SX₈X₉AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein
- 25 HGNFGNSYISYWAY is most preferred.
- [108]** For X₁, the amino acid V is preferred. For X₂, the amino acid K is most preferred, and for X₃, the amino acid M is most preferred. A preferred combination for X₂ and X₃ is M for X₃ in combination with any of the amino acid residues of X₂, such as the combinations for X₂ and X₃, respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X₂ and X₃, respectively.
- 30 Preferred examples of said CDR-H1 sequence X₂YAX₃N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is more preferred, wherein KYAMN is most preferred. For X₄, the amino acid S is preferred. For X₅, the amino acid D is most preferred. A preferred combination is S for X₄ in combination with
- 35 any of the amino acid residues of X₅, such as the combinations for X₄ and X₅, respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₄VKX₅ are selected

from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD is more preferred, wherein RIRSKYNNYATYYADSVKD is most preferred. For X_6 , the amino acid G is most preferred; for X_7 , the amino acid I is most preferred; for X_8 , the amino acid Y is most preferred; and for X_9 , the amino acid W is most preferred. Preferred examples of said CDR-H3 sequence $HX_6NFGNSYX_7SX_8X_9AY$ are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[109] The VL region of ii) comprises or consists of the sequence of QTVVTQEPLTVSPGGTVTLTCX₁SSTGAVTSGX₂YPNWWQQKPGQAPRGLIGX₃TX₄X₅X₆X₇X₈GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCX₉LWYSNRWWFGGGTKLTVL, where X_1 is G, R, or A; X_2 is N or Y; X_3 is G or A; X_4 is K or D; X_5 is F or M; X_6 is L or R; X_7 is A, P or V; X_8 is P or S; and X_9 is V, A, or T.

[110] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of X_1 SSTGAVTSGX₂YPN; a CDR-L2 sequence comprising or consisting of X_3 TX₄X₅X₆X₇X₈; and a CDR-L3 sequence comprising or consisting of X_9 LWYSNRWW. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, TLWYSNRWW, and ALWYSNLWW, wherein VLWYSNRWW is most preferred.

[111] For X_1 , the amino acid G is most preferred. For X_2 , the amino acid N is preferred. X_1 and X_2 are part of the CDR-L1 sequence X_1 SSTGAVTSGX₂YPN within the VL region. Preferred examples of said CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. For X_3 , the amino acid G is preferred. For X_4 , the amino acid K is preferred. For X_5 , the amino acid F is preferred. For X_6 , the amino acid L is preferred. For X_7 , the amino acid A is most preferred. For X_8 , the amino acid P is preferred. X_3 to X_8 are part of the CDR-L2 sequence X_3 TX₄X₅X₆X₇X₈ of the VL region. Preferred examples of said CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. For X_9 , the amino acid V is most preferred. X_9 is part of the CDR-L3 sequence

X₉LWYSNRWV of the VL region. Preferred examples of said CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, TLWYSNRWV, and ALWYSNLWV, wherein VLWYSNRWV is most preferred.

[112] In another preferred embodiment, the VH region of ii) comprises or consists of the sequence

EVQLVESGGGLX₁QPGGSLKLSCAASGFTFNX₂YAX₃NWVRQAPGKGLEWVARIRSKYNNY
ATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYW
GGGTLTVSS, where X₁ is V or E; X₂ is K, V, S, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G, K or S; X₆ is G or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F; and the VL region of
ii) comprises or consists of the sequence
QTVVTQEPSLTVSPGGTVTLTCX₁SSTGAVTSGX₂YPNWWQQKPGQAPRGLIGGTKFLX₃PG
TPARFSGSLLGGKAAALTLSGVQPEDEAEYYCX₄LWYSNRWVFGGGTKLTVL, where X₁ is G or A; X₂ is N or Y; X₃ is A or V; and X₄ is V, A, or T.

[113] The VH region of ii) comprises or consists of the sequence of
EVQLVESGGGLX₁QPGGSLKLSCAASGFTFNX₂YAX₃NWVRQAPGKGLEWVARIRSKYNNY
ATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYW
GGGTLTVSS, where X₁ is V or E; X₂ is K, V, S, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G, K or S; X₆ is G or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F.

[114] The CDR sequences within said VH region are as follows: a CDR-H1 sequence comprising or consisting of X₂YAX₃N; a CDR-H2 sequence comprising or consisting of RIRSKYNNYATYYADX₄VKX₅; and a CDR-H3 sequence comprising or consisting of HX₆NFGNSYX₇SX₈X₉AY. Preferred examples of said CDR-H1 sequence X₂YAX₃N are selected from KYAMN, VYAMN, SYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN are more preferred, wherein KYAMN is most preferred. Preferred examples of said

CDR-H2 sequence RIRSKYNNYATYYADX₄VKX₅ are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD are more preferred, wherein RIRSKYNNYATYYADSVKD is most preferred. Preferred examples of said CDR-H3
sequence HX₆NFGNSYX₇SX₈X₉AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY or HANFGNSYISYWAY are more preferred, wherein HGNFGNSYISYWAY is most preferred.

[115] For X₁, the amino acid V is preferred. For X₂, the amino acid K is most preferred, and for X₃, the amino acid M is most preferred. A preferred combination for X₂ and X₃ is M for X₃

- in combination with any of the amino acid residues of X_2 , such as the combinations for X_2 and X_3 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_2 and X_3 , respectively. Preferred examples of said CDR-H1 sequence X_2YAX_3N are selected from KYAMN, VYAMN, SYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN are more preferred, wherein KYAMN is most preferred. For X_4 , the amino acid S is preferred. For X_5 , the amino acid D is most preferred. A preferred combination is S for X_4 in combination with any of the amino acid residues of X_5 , such as the combinations for X_4 and X_5 , respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D.
- Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYAD X_4 VK X_5 are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD are more preferred, wherein RIRSKYNNYATYYADSVKD is most preferred are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred. For X_6 , the amino acid G is most preferred; for X_7 , the amino acid I is most preferred; for X_8 , the amino acid Y is most preferred; and for X_9 , the amino acid W is most preferred. Preferred examples of said CDR-H3 sequence H X_6 NFGNSY X_7 S X_8 X_9 AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.
- [116] The VL region of ii) comprises or consists of the sequence of QTVVTQEPSLTVSPGGTVTLTC X_1 SSTGAVTSG X_2 YPNWWQQKPGQAPRGLIGGTKFL X_3 PGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC X_4 LWYSNRWWFGGGTKLTVL, where X_1 is G or A; X_2 is N or Y; X_3 is A or V; and X_4 is V, A, or T.
- [117] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of X_1 SSTGAVTSG X_2 YPN; a CDR-L2 sequence comprising or consisting of GTKFL X_3 P; and a CDR-L3 sequence comprising or consisting of X_4 LWYSNRWW. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, TLWYSNRWW, and

ALWYSNLWV, wherein VLWYSNRWV is most preferred.

[118] For X_1 , the amino acid G is preferred. For X_2 , the amino acid N is preferred. X_1 and X_2 are part of the CDR-L1 sequence X_1 SSTGAVTSG X_2 YPN within the VL region. Preferred examples of said CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. X_3 is part of the CDR-L2 sequence GTKFL X_3 P of the VL region. Said CDR-L2 sequence can either be GTKFLAP or GTKFLVP, wherein GTKFLAP is preferred. For X_3 , the amino acid A is preferred. X_4 is part of the CDR-L3 sequence X_4 LWYSNRWV of the VL region. Preferred examples of said CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, and TLWYSNRWV, wherein VLWYSNRWV is most preferred. For X_4 , the amino acid V is most preferred.

[119] In a further preferred embodiment, the VH region of i) comprises or consists of the sequence of
 EVQLVESGGGLVQPGGSLKLSCAASGFTFN X_1 YAMNWVRQAPGKGLEWWARIRSKYNNYA
 TYYADSVK X_2 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY X_3 S X_4 WAYWGQ
 GTLVTVSS, where X_1 is K or S; X_2 is D or G; X_3 is I or V; and X_4 is Y or W; and the VL region of ii) comprises or consists of the sequence of
 QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG X_1 YPNWWQQKPGQAPRGLIGGTKFLAPGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYC X_2 LWYSNRWVFGGGTKLTVL, where X_1 is N or Y; and X_2 is V or A.

[120] The VH region of i) comprises or consists of the sequence of
 EVQLVESGGGLVQPGGSLKLSCAASGFTFN X_1 YAMNWVRQAPGKGLEWWARIRSKYNNYA
 TYYADSVK X_2 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY X_3 S X_4 WAYWGQ
 GTLVTVSS, where X_1 is K or S, wherein K is preferred; X_2 is D or G, wherein D is preferred; X_3 is I or V, wherein I is preferred; and X_4 is Y or W, wherein Y is preferred.

[121] The CDR sequences within said VH region are as follows: a CDR-H1 sequence comprising or consisting of X_1 YAMN; a CDR-H2 sequence comprising or consisting of RIRSKYNNYATYYADSVK X_2 ; and a CDR-H3 sequence comprising or consisting of HGNFGNSY X_3 S X_4 WAY. Said CDR-H1 sequence X_1 YAMN is selected from KYAMN or SYAMN, wherein KYAMN is preferred. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADSVK X_2 are selected from RIRSKYNNYATYYADSVKD and RIRSKYNNYATYYADSVKG, wherein RIRSKYNNYATYYADSVKD is preferred. Said CDR-H3 sequence HGNFGNSY X_3 S X_4 WAY is HGNFGNSYISYWAY or HGNFGNSYVSWWAY, wherein HGNFGNSYISYWAY is preferred.

[122] The VL region of ii) comprises or consists of the sequence of
 QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG X_1 YPNWWQQKPGQAPRGLIGGTKFLAPGT

PARFSGSLLGGKAALTLSGVQPEDEAEYYCX₂LWYSNRWWFGGGTKLTVL, where X₁ is N or Y, wherein N preferred; and X₂ is V or A, wherein V preferred.

[123] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of GSSTGAVTSGX₁YPN; a CDR-L2 sequence comprising or consisting of GTKFLAP; and a CDR-L3 sequence comprising or consisting of X₂LWYSNRWW. The CDR-L1 sequence is GSSTGAVTSGNYPN or GSSTGAVTSGYYPN, wherein GSSTGAVTSGNYPN is preferred. The CDR-L3 sequence is VLWYSNRWW or ALWYSNRWW, wherein VLWYSNRWW is preferred.

[124] In a preferred embodiment, the VH region of i) comprises or consists of the sequence as defined in SEQ ID NOs: 124, 172, 362, 552, 730, 928, 1106, 1296, 1474, 1664 or 1854; and the VL region of ii) comprises or consists of the sequence of as defined in SEQ ID NOs: 125, 173, 363, 553, 731, 929, 1107, 1297, 1475, 1665, or 1855. Preferred combinations of VH and VL regions of i) and ii) are defined in SEQ ID NOs: 124 and 125 (combination of binder termed "2B2"), 172 and 173 ("A2J"), 362 and 363 ("E1L"), 552 and 553 ("E2M"), 730 and 731 ("F12Q"), 928 and 929 ("F6A"), 1106 and 1107 ("F7O"), 1296 and 1297 ("G4H"), 1474 and 1475 ("H1E"), 1664 and 1665 ("H2C"), or 1854 and 1855 ("I2C"). Preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 172 and 173, 362 and 363, 552 and 553, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855. More preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 362 and 363, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855. Even more preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 730 and 731, 1664 and 1665, and 1854 and 1855. In a yet even more preferred embodiment, the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 730 and 731, 1664 and 1665, and 1854 and 1855.

[125] In the most preferred embodiment, the VH region of i) comprises or consists of the sequence of

EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNYA
 TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LVTVSS (SEQ ID NO: 1854); and the VL region of ii) comprises or consists of the sequence of

QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGGTKFLAPGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL (SEQ ID NO:

1855).

[126] As outlined herein above in relation to amino acid substitutions in the CDR sequences and also applying to this embodiment, the VH region of i) and/or VL region of ii) comprise one or more amino acid substitutions as specified herein above. Accordingly, at least one of the recited amino acid substitutions of the variable regions is comprised in said binding domain binding to an extracellular epitope of the human CD3 ϵ chain. Said at least one or one or more amino acid substitution, in the case that only one amino acid substitution is present, can be present in a CDR sequence in said VH or said VL region or, in case more than one amino acid substitution is present, in CDRs in both the VH and the VL region or restricted to CDR sequences in only the VH or the VL region. In certain embodiments where there are more than one amino acid substitutions, the substitutions are in the VH and the VL region or, alternatively, only in one variable region. Preferably, the substitutions are in the VH and the VL region.

[127] Specifically, the VH of i) and/or VL region sequence of ii) comprises one or more amino acid substitutions selected from

- a. N30 (preferably S), X₆34V, X₆34F, Q39 (E, K, R, D, preferably E), L45 (M or V, preferably M), D64 (preferably E), X₇65A, X₁₂81V, X₁₂81T, X₁₂81I, V99 (A or L, preferably A), H101 (preferably A or N), X₁₄102E, F104 (preferably I), N106 (preferably S or T) in the VH region sequence in i); and
- b. L20 (preferably I or M), V38 (I, L, M, F or Y, preferably I), X₁₁40R, X₁₁40K, X₂₄69 (S or E, preferably S), X₃₂91L, X₃₃93 (preferably Y), G102 (preferably S) in the VL region sequence in ii).

[128] In the VH region sequence, the amino acid substitution at position 30 is, preferably, S (hence, can be written as N30S; same is true for the subsequent substitutions given according to their position number). The amino acid substitution at position 34 is V or F. Preferably, position 34 of the VH region sequence comprises an I or M, most preferred an I. The amino acid substitution at position 39 is E, K, R, D, preferably E. The amino acid substitution at position 45 is preferably M or V, more preferred M. The amino acid substitution at position 64 is preferably E. The amino acid substitution at position 65 is A. The amino acid substitution at position 81 is V, T or I, preferably V. The amino acid substitution at position 99 is preferably A or L, more preferred A. The amino acid substitution at position 101 is preferably A or N, more preferred A (H1A). The amino acid substitution at position 102 is E. The amino acid substitution at position 104 is preferably I. The amino acid substitution at position 106 is preferably S or T, more preferred S.

[129] Notwithstanding the above, in the CDR-H2 sequence within the VH region sequence, the amino acid substitution at position 64 is, preferably, D15E, or the amino acid substitution

- at position 65 with amino acid A. Preferably, said CDR-H2 comprises the amino acid residue substitution at position 65 with amino acid A; in this case, a preferred amino acid for the last amino acid of CDR-H2 is D or G, preferred D. Hence, a preferred CDR-H2 sequence is RIRSKYNNYATYYADAVKD or RIRSKYNNYATYYADAVKG, with
- 5 RIRSKYNNYATYYADAVKD more preferred. In case CDR-H2 contains two amino acid substitutions, the combination of the amino acid E at position 64 and amino acid A at position 64 are preferred; in this case, a preferred amino acid for the last amino acid of CDR-H2 is G. Hence, a preferred CDR-H2 sequence for the combination of the amino acid E at position 64 and amino acid A at position 65 is RIRSKYNNYATYYAEAVKG.
- 10 **[130]** In the CDR-H3 sequence of the VH sequence, the amino acid substitutions are at position 101, preferably a substitution with amino acid A or N, more preferably A, at position 102 with amino acid E, at position 104, preferably with amino acid I, and at position 106, preferably with amino acid S or T. Preferably, CDR-H3 comprises the amino acid A or N at position 101, the amino acid S or T at position 106; in this case and if placeholders are
- 15 present in the CDR-H3 sequence at the indicated positions, preferred amino acids for X_{14} are G or A, most preferred G; for X_{15} is I; for X_{16} is Y; and for X_{17} are W or Y. In case CDR-H3 comprises two amino acid substitutions, preferred combinations are the amino acid A at position 101 and the amino acid S at position 106; and the amino acid N at position 101 and the amino acid T at position 106; in this case and if placeholders are present in the CDR-H3
- 20 sequence at the indicated positions, a preferred amino acid for X_{14} is G or A, most preferred G; for X_{15} is I, for X_{16} is Y, and for X_{17} are W and F. In case CDR-H3 comprises three amino acid substitutions, preferred combinations are the amino acid A at position 101, the amino acid I at position 104, and the amino acid S at position 106; and the amino acid N at position 101, the amino acid I at position 104 and the amino acid T at position 106, in this case and if
- 25 placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_{15} is I, for X_{16} is Y, and for X_{17} are W and F. In case CDR-H3 comprises four amino acid substitutions, a preferred combination is the amino acid N at position 101, the amino acid E at position 102, the amino acid I at position 104, and the amino acid T at position 106; in this case and if placeholders are present in the CDR-H3 sequence at the
- 30 indicated positions, a preferred amino acid for X_{15} is I, for X_{16} is Y, and for X_{17} is W. Hence, preferred CDR-H3 sequences are selected from AGNFGSSYISYWAY, NENIGTSYISYWAY, AGNFGTSYISYWAY, NANFGTSYISYFAY, and AGNFGSSYISYFAY, with AGNFGSSYISYWAY and AGNFGSSYISYFAY most preferred.
- [131]** In the VL region sequence, the amino acid substitution at position 20 is preferably I or
- 35 M, more preferred I. The amino acid substitution at position 38 is preferably I, L, M, F or Y, more preferred with I. The amino acid substitution at position 40 is preferably K or R, more preferred K. The amino acid substitution at position 69 is preferably S or E, more preferred S.

The amino acid substitution at position 91 is L. The amino acid substitution at position 93 is preferably Y. The amino acid substitution at position 102 is preferably S.

[132] Notwithstanding the above, in the CDR-L3 sequence within the VL region sequence, the amino acid substitution at position 1 is with amino acid L or the amino acid substitution is W93, preferably W93Y. Preferably, the CDR-L3 sequence is VLYYSNRWW when CDR-L3 comprises an amino acid substitution. It is preferred, however, that CDR-L3 does not comprise said X₁L and W93 amino acid substitution, in which case a preferred CDR-L3 sequence is VLYYSNRWW.

[133] In accordance with the foregoing, the amino acid substitution H101A in the VH region (part of CDR-H3) is preferably the amino acid substitution, in case there is only one amino acid substitution present in the CD3epsilon binding domain, within the VH and/or VL region sequences as defined herein. Furthermore, in case of combinations of amino acid substitutions as defined in iii) preferably H101A in the VH region sequence is one of the amino acid substitutions of said combination.

[134] In a preferred embodiment of the polypeptide or polypeptide construct of the invention, wherein in addition to said one amino acid substitution or a combination thereof as defined in iii) X₆ is I; X₈ is G; X₁₂ is L, X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence. In a preferred embodiment of the polypeptide or polypeptide construct of claim 1 of the invention, in addition to said one amino acid substitution or a combination thereof as defined in iii) X₆ is I; X₈ is G; X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence. The one amino acid substitution or combination thereof as defined herein is/are in addition combined with specific amino acids at specific positions in the CDRs. Hence, at least one of the recited amino acid substitutions in accordance with iii) is present and at least one of X₈ is G; X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence is additionally present in the CDRs. As previously stated herein above, a preferred amino acid for X₆ is I or X₈ is G in said VH region sequence, if only one additional amino acid is present in the CDRs, wherein it is most preferred that X₅ is I in said VH region sequence. A preferred combination of two of said additional amino acids is X₆ is I and X₁₇ is F in said VH region sequence; or X₈ is G and X₁₇ is F in said VH region sequence. A preferred combination of three of said additional amino acids is X₆ is I, X₁₄ is A, and X₁₇ is F in said VH region sequence; or X₆ is I, X₁₇ is F in said VH region sequence, and X₃₂ is A in said VL region sequence. Since the latter amino acids are to be present additionally, it is understood that those recited additional amino acids that overlap in position with the amino acid substitution of iii) cannot replace the overlapping amino acid substitution. For example, if the only amino acid substitution in accordance with iii) is either X₆34V or X₆34F in CDR-H1, said amino acid cannot be replaced by amino acid I in said CDR-H1 sequence, since there would be no amino acid substitution as defined in iii)

remaining in the binding domain. In other terms, there must always be at least one of the amino acid substitutions as defined in iii) comprised in the polypeptide or polypeptide construct of the invention.

[135] It is also understood that depending on the actual sequence of the VH and/or VL region sequences, one or more of said additional amino acids may already be part of the given variable sequence as defined herein above or, if this is not the case, said given variable region will be changed to exhibit said additional amino acid(s) in combination with one amino acid substitution or a combination thereof as recited in iii).

[136] In a preferred embodiment of the polypeptide or polypeptide construct of the invention, it comprises combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more amino acid substitutions.

[137] In a preferred embodiment of the polypeptide or polypeptide construct of the invention, i) said one acid substitution is selected from a. X₆₃₄V, Q39E, Q39K, Q39R, Q39D, L45M, L45V, X₁₂₈₁V, X₁₂₈₁T, X₁₂₈₁I, V99A, V99L, H101A, H101N in the VH region; and b. V38I, V38L, V38M, V38F, V38Y, X₁₁₄₀R, X₁₁₄₀K, X₂₄₆₉S, X₂₄₆₉E, X₃₂₉₁L, X₃₃₉₃Y; ii) said combination of two or more amino acid substitutions are selected from X₆₃₄F and A81V (which may also be referred to as X₁₂₈₁V) in the VH region; Q39E in the VH region and X₁₁₄₀K in the VL region; Q39E in the VH region and X₁₁₄₀R in the VL region; Q39D in the VH region and X₁₁₄₀K in the VL region; Q39D in the VH region and X₁₁₄₀R in the VL region; L45V in the VH region and V38F in the VL region; L45V in the VH region and V38Y in the VL region; L45M in the VH region and X₁₁₄₀K in the VL region; L20I and G102S in the VL region; A81V in the VH region and X₁₁₄₀K in the VL region; iii) said combination of three or more amino acid substitutions are selected from Q39E in the VH region, X₁₁₄₀K and G102S in the VL region; Q39E in the VH region, X₁₁₄₀R and G102S in the VL region; Q39D in the VH region, X₁₁₄₀K and G102S in the VL region; Q39D in the VH region, X₁₁₄₀R and G102S in the VL region; L45M in the VH region, X₁₁₄₀K and G102S in the VL region; X₇₆₅A, H101A, and N106S in the VH region; L20I, X₁₁₄₀K, and G102S in the VL region; iv) said combination of four or more amino acid substitutions are selected from Q39E in the VH region, L20I, X₁₁₄₀K and G102S in the VL region; Q39E in the VH region, L20I, X₁₁₄₀R and G102S in the VL region; Q39D in the VH region, L20I, X₁₁₄₀K and G102S in the VL region; Q39D in the VH region, L20I, X₁₁₄₀R and G102S in the VL region; L45M in the VH region, L20I, X₁₁₄₀K and G102S in the VL region; L20I, X₁₁₄₀K, X₂₄₆₉S, and G102S in the VL region; A81V in the VH region, L20I, X₁₁₄₀K, and G102S in the VL region; and/or v) said combination of five, six, seven, eight, nine, ten, or more amino acid substitutions are selected from X₇₆₅A, A81V, V99A, N106S in the VH region, L20I, X₁₁₄₀K, X₂₄₆₉S, and G102S in the VL region; D64E, X₇₆₅A, A81V, X₁₄₁₀₂E, F104I, N106T in the VH region, L20I, X₂₄₆₉S, and G102S in the VL region; L45M, X₇₆₅A, N106T in the VH region, L20I, X₁₁₄₀K, X₂₄₆₉S, and G102S in the VL

region; X₇65A, A81V, V99A, H101A, F104I, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₇65A, A81V, V99A, H101A, N106S in the VH region; A81V, V99A in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; Q39E, A81V in the VH region, L20I, X₁₁40K, and G102S in the VL region; L45V in the VH region, L20I, V38F, X₁₁40K and G102S in the VL region.

[138] In a more preferred embodiment of the polypeptide or polypeptide construct of the invention, said combination of amino acid substitutions is selected from:

i) in the VH region

- a. X₇65A, A81V, V99A, H101A and N106S;
- 10 b. D64E, X₇65A, A81V, H101N, X₁₄102E, F104I, and N106S;
- c. L45M, X₇65A, H101A, and N106T;
- d. L45M, X₇65A, H101A, and N106S;
- e. Q39E, X₇65A, H101N, and N106T;
- f. D64E, X₇65A, V99A, H101A, and N106T;
- 15 g. X₇65A, A81V, V99A, H101A, X₁₄102E, F104I, and N106T;
- h. X₇65A, A81V, H101N, X₁₄102E, F104I, and N106S;
- i. D64E, X₇65A, A81V, H101A, and N106S;
- j. D64E, X₇65A, H101A, and N106T;
- k. X₇65A, V99A, H101A, and N106T;
- 20 l. D64E, X₇65A, H101A, and N106S;
- m. D64E, X₇65A, A81V, V99A, H101A, and N106S;
- n. X₇65A, H101A and N106S;
- o. N30S, Q39E, D64E, X₇65A, A81V, H101A, X₁₄102E, F104I, and N106T;
- p. L45M, D64E, X₇65A, H101A, and N106T;
- 25 q. N30S, L45M, X₇65A, A81V, H101A, and N106T;
- r. N30S, L45M, D64E, X₇65A, A81V, H101A, and N106S;

ii) in the VL region

- a. L20I, X₁₁40K, X₂₄69S, and G102S;
- b. L20I, X₂₄69S, and G102S;
- 30 c. L20I, V38I, X₁₁40K, X₂₄69E, G102S and W93Y;
- d. X₁₁40K and G102S;
- e. L20I, X₁₁40K, X₂₄69S, G102S and W93Y;
- f. L20M, X₁₁40K and X₂₄69E;
- g. L20I, V38I, X₁₁40K, X₂₄69E and G102S;
- 35 h. X₁₁40K, X₂₄69S and W93Y;
- i. X₁₁40K and X₂₄69S; and

iii) a combination of one amino acid substitution combination of i) and ii).

[139] In yet another preferred embodiment of the polypeptide or polypeptide construct of the invention, said combination of amino acid substitution combinations of iii) is selected from:

- a. X₇65A, A81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- b. D64E, X₇65A, A81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- c. L45M, X₇65A, H101A, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- d. L45M, X₇65A, H101A, N106S in the VH region, L20I, V38I, X₁₁40K, X₂₄69E, G102S and W93Y in the VL region;
- e. Q39E, X₇65A, H101N, N106T in the VH region, X₁₁40K and G102S in the VL region;
- f. D64E, X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- g. X₇65A, A81V, V99A, H101A, X₁₄102E, F104I, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- h. X₇65A, A81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- i. D64E, X₇65A, A81V, H101A, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- j. D64E, X₇65A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- k. X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- l. D64E, X₇65A, H101A, N106S in the VH region, X₁₁40K and G102S in the VL region;
- m. D64E, X₇65A, A81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, G102S and W93Y in the VL region;
- n. X₇65A, H101A N106S in the VH region, X₁₁40K and G102S in the VL region;
- o. N30S, Q39E, D64E, X₇65A, A81V, H101A, X₁₄102E, F104I, N106T in the VH region, L20M, X₁₁40K and X₂₄69E in the VL region;
- p. L45M, D64E, X₇65A, H101A, N106T in the VH region, L20I, V38I, X₁₁40K, X₂₄69E and G102S in the VL region;
- q. N30S, L45M, X₇65A, A81V, H101A, N106T in the VH region, X₁₁40K and X₂₄69S in the VL region; and

- r. N30S, L45M, D64E, X₇65A, A81V, H101A, N106S in the VH region, X₁₁40K and X₂₄69S in the VL region.

[140] In another preferred embodiment of the polypeptide or polypeptide construct of the invention, in said combination of amino acid substitution combinations defined in:

- a. and m. X₆ is I in said VH region sequence;
- b. and r. X₈ is G in said VH region sequence;
- c. X₁₂ is L in said VH region;
- d. X₁₂ is L and X₁₇ is F in said VH region;
- 10 e. X₆ is I, X₁₄ is A and X₁₇ is F in said VH region sequence;
- f. X₆ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
- g. X₆ is I in said VH region sequence;
- h. and i. X₈ is G in said VH region sequence;
- j., l. and n. X₆ is I and X₁₇ is F in said VH region sequence; and X₃₂ is A in said VL region sequence;
- 15 k. X₆ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
- p. X₁₂ is L in said VH region; or
- q. X₈ is G and X₁₇ is F in said VH region sequence.

Examples of VH and VL region sequences as defined in this embodiment are defined by SEQ ID NOs: 2012 and 2013; 2020 and 2021; 2028 and 2029; 2036 and 2037; 2044 and 2045; 26 and 27; 34 and 35; 42 and 43; 50 and 51; 58 and 59; 66 and 67; 74 and 75; 82 and 83; 90 and 91; 98 and 99; 100 and 101; 108 and 109; 116 and 117. Table 2 evidences the increase of the aforementioned VH and VL region sequence combinations of the CD3ε binding domain in temperature stability over the CD3ε binding domain comprising a VH and VL combination defined as "I2C" (SEQ ID NOs: 1854 and 1855, respectively).

[141] In accordance with the invention, the binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3ε chain and comprising or consisting of a VH region and a VL region as defined herein comprises at least one of the following CDR sequences or a combination thereof as defined in SEQ ID NOs: 1878, 1908, 1989, and 2003. Said sequences contain one amino acid substitution or a combination thereof as defined in iii), and in some instances also said additional amino acids as defined herein above. Preferred combinations of said CDR sequences are listed in the following in the order of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3: 1878 to 1883; 1908 to 1913; 1984 to 1989; 1998 to 2003.

[142] Also in accordance with the invention are CDR sequence combinations in the order of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3 as defined in SEQ ID NOs: 126 to 131; 134 to 139; 142 to 147; 150 to 155; 158 to 163.

[143] Also in accordance with the invention and more preferred are CDR sequence combinations as defined in SEQ ID NOs (listed in the order of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3): 2006 to 2011; 2014 to 2019; 2022 to 2027; 2030 to 2035; 2038 to 2043; 20 to 25; 36 to 41; 44 to 49; 52 to 57; 60 to 65; 68 to 73; 76 to 81; 84 to 89; 92 to 97; 102 to 107; 110 to 115. Further examples are SEQ ID NOs: 282 to 287; 290 to 295; 298 to 303; 306 to 311; 314 to 319; 472 to 477; 480 to 485; 488 to 493; 496 to 501; 504 to 509; 650 to 655; 658 to 663; 666 to 671; 674 to 679; 682 to 687; 840 to 845; 848 to 853; 856 to 861; 864 to 869; 872 to 877; 1026 to 1031; 1034 to 1039; 1042 to 1047; 1050 to 1055; 1058 to 1063; 1216 to 1221; 1224 to 1229; 1232 to 1237; 1240 to 1245; 1248 to 1253; 1394 to 1399; 1402 to 1407; 1410 to 1415; 1418 to 1423; 1426 to 1431; 1584 to 1589; 1592 to 1597; 1600 to 1605; 1608 to 1613; 1616 to 1621; 1774 to 1779; 1782 to 1787; 1790 to 1795; 1798 to 1803; 1806 to 1811;

[144] In accordance with the invention, the binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain comprises or consists of a VH region sequence as defined in the following SEQ ID NOs: 1856, 1860, 1862, 1864, 1872, 1884, 1894, 1896, 1898, 1900, 1902, 1904, 1906, 1914, 1916, 1918, 1920, 1922, 1924, 1926, 1928, 1930, 1932, 1934, 1936, 1938, 1940, 1942, 1944, 1946, 1948, 1950. Said sequences contain one amino acid substitution or a combination thereof as defined herein above, and in some instances also said additional amino acids as defined herein above. This is also true for the below embodiments characterizing by sequence ID number CD3epsilon binding domains that result from amino acid residue exchanges as specified herein.

[145] In accordance with the invention, the binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain comprises or consists of a VL region sequence as defined in the following SEQ ID NOs: 1867, 1869, 1871, 1875, 1877, 1899, 1901, 1903, 1905, 1907, 1919, 1921, 1923, 1925, 1927, 1929, 1931, 1933, 1935, 1937, 1939, 1941, 1943, 1961, 1963, 1965, 1967, 1969, 1971, 1975, 1991, 1993, 1995, 1997, or 2005.

[146] Preferred combinations of VH and VL region sequences of said binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain are defined in the following SEQ ID NOs: 1856 and 1857; 1860 and 1861; 1862 and 1863; 1864 and 1865; 1866 and 1867; 1868 and 1869; 1870 and 1871; 1872 and 1873; 1874 and 1875; 1876 and 1877; 1884 and 1885; 1894 and 1895; 1896 and 1897; 1898 and 1899; 1900 and 1901; 1902 and 1903; 1904 and 1905; 1906 and 1907; 1914 and 1915; 1916 and 1917; 1918 and 1919; 1920 and 1921; 1922 and 1923; 1924 and 1925; 1926 and 1927; 1928 and 1929; 1930 and 1931; 1932 and 1933; 1934 and 1935; 1936 and 1937; 1938 and 1939; 1940 and 1941; 1942 and 1943; 1944 and 1945; 1946 and 1947; 1948 and

1949; 1950 and 1951; 1960 and 1961; 1962 and 1963; 1964 and 1965; 1966 and 1967; 1968 and 1969; 1970 and 1971; 1974 and 1975; 1990 and 1991; 1992 and 1993; 1994 and 1995; 1996 and 1997; or 2004 and 2005.

5 **[147]** Also in accordance with the invention are VH region sequences as defined in SEQ ID NO: 132, 140, 148, 156, and 164.

[148] Also in accordance with the invention are VL region sequences as defined in SEQ ID NO: 133, 141, 149, 157, and 165.

10 **[149]** Also in accordance with the invention are any combinations of the foregoing particularly preferred VH and VL region sequences. Preferred are the following VH and VL combinations as defined by SEQ ID NOs: 132 and 133; 140 and 141; 148 and 149; 156 and 157; and 164 and 165.

[150] Also in accordance with the invention and more preferred are VH region sequences as defined in SEQ ID NO: 2012, 2020, 2028, 2036, 2044, 26, 34, 42, 50, 58, 66, 74, 82, 90, 98, 100, 108, and 116. Further examples are SEQ ID NOs: 288, 296, 304, 312, 320, 478, 15 486, 494, 502, 510, 656, 664, 672, 680, 688, 846, 854, 862, 870, 878, 1032, 1040, 1048, 1056, 1064, 1222, 1230, 1238, 1246, 1254, 1400, 1408, 1416, 1424, 1432, 1590, 1598, 1606, 1614, 1622, 1780, 1788, 1796, 1804, and 1812.

20 **[151]** Also in accordance with the invention and more preferred are VL region sequences as defined in SEQ ID NO: 2013, 2021, 2029, 2037, 2045, 27, 35, 43, 51, 59, 67, 75, 83, 91, 99, 101, 109, and 117. Further examples are SEQ ID NOs: 289, 297, 305, 313, 321, 479, 487, 495, 503, 511, 657, 665, 673, 681, 689, 847, 855, 863, 871, 879, 1033, 1041, 1049, 1057, 1065, 1223, 1231, 1239, 1247, 1255, 1401, 1409, 1417, 1425, 1433, 1591, 1599, 1607, 1615, 1623, 1781, 1789, 1797, 1805, and 1813.

25 **[152]** Also in accordance with the invention and preferred are any combinations of the foregoing particularly preferred VH and VL region sequences. Preferred are the following VH and VL combinations as defined by SEQ ID NOs: 2012 and 2013; 2020 and 2021; 2028 and 2029; 2036 and 2037; 2044 and 2045; 26 and 27; 34 and 35; 42 and 43; 50 and 51; 58 and 59; 66 and 67; 74 and 75; 82 and 83; 90 and 91; 98 and 99; 100 and 101; 108 and 109; and 116 and 117. Further examples are SEQ ID NOs: 288 and 289; 296 and 297; 304 and 305; 30 312 and 313; 320 and 321; 478 and 479; 486 and 487; 494 and 495; 502 and 503; 510 and 511; 656 and 657; 664 and 665; 672 and 673; 680 and 681; 688 and 689; 846 and 847; 854 855; 862 and 863; 870 and 871; 878 and 879; 1032 and 1033; 1040 and 1041; 1048 and 1049; 1056 and 1057; 1064 and 1065; 1222 and 1223; 1230 and 1231; 1238 and 1239; 1246 and 1247; 1254 and 1255; 1400 and 1401; 1408 and 1409; 1416 and 1417; 1424 and 1425; 35 1432 and 1433; 1590 and 1591; 1598 and 1599; 1606 and 1607; 1614 and 1615; 1622 and 1623; 1780 and 1781; 1788 and 1789; 1796 and 1797; 1804 and 1805; and 1812 and 1813.

[153] In accordance with the invention, said binding domain of the polypeptide or

polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain comprises or consists of a VH region sequence selected from SEQ ID NOs: 2012, 2020, 2028, 2036, 2044, 26, 34, 42, 50, 58, 66, 74, 82, 90, 98, 100, 108, 116, 288, 296, 304, 312, 320, 478, 486, 494, 502, 510, 656, 664, 672, 680, 688, 846, 854, 862, 870, 5 878, 1032, 1040, 1048, 1056, 1064, 1222, 1230, 1238, 1246, 1254, 1400, 1408, 1416, 1424, 1432, 1590, 1598, 1606, 1614, 1622, 1780, 1788, 1796, 1804, 1812, 1856, 1860, 1862, 1864, 1872, 1884, 1894, 1896, 1898, 1900, 1902, 1904, 1906, 1914, 1916, 1918, 1920, 1922, 1924, 1926, 1928, 1930, 1932, 1934, 1936, 1938, 1940, 1942, 1944, 1946, 1948, 1950, 132, 140, 148, 156, and 164; and/or a VL region sequence selected from SEQ ID NOs: 10 2013, 2021, 2029, 2037, 2045, 27, 35, 43, 51, 59, 67, 75, 83, 91, 99, 101, 109, and 117, 289, 297, 305, 313, 321, 479, 487, 495, 503, 511, 657, 665, 673, 681, 689, 847, 855, 863, 871, 879, 1033, 1041, 1049, 1057, 1065, 1223, 1231, 1239, 1247, 1255, 1401, 1409, 1417, 1425, 1433, 1591, 1599, 1607, 1615, 1623, 1781, 1789, 1797, 1805, 1813, 1867, 1869, 1871, 1875, 1877, 1899, 1901, 1903, 1905, 1907, 1919, 1921, 1923, 1925, 1927, 1929, 1931, 15 1933, 1935, 1937, 1939, 1941, 1943, 1961, 1963, 1965, 1967, 1969, 1971, 1975, 1991, 1993, 1995, 1997, 2005, 133, 141, 149, 157, and 165.

[154] According to the invention, it is preferred that the polypeptide or polypeptide construct comprises: a binding domain binding to an extracellular epitope of the human CD3 ϵ chain comprising or consisting of i) a VH region and ii) a VL region, wherein said VH and VL region 20 of i) and ii) is selected from the VH and VL region combination as defined in SEQ ID NOs: 124 and 125, 172 and 173, 362 and 363, 552 and 553, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855, wherein said one amino acid substitution or a combination thereof in said VH and/or VL region sequence results in a VH and/or a VL region sequence having the amino acid residue:

- 25 i. I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, and S at position 102 in the VL region sequence;
M at position 45, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
30 M at position 45, A at position 65, L at position 81, A at position 101, S at position 106, F at position 112 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69, S at position 102 and Y at position 93 in the VL region sequence;
35 I at position 34, E at position 39, A at position 65, N at position 101, A at position 102, T at position 106, F at position 112 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;

- I at position 34, E at position 64, A at position 65, A at position 99, A at position 101, T at position 106 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
- I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
- E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;
- I at position 34, E at position 64, A at position 65, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
- I at position 34, E at position 64, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
- I at position 34, E at position 64, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, S at position 102 and Y at position 93 in the VL region sequence;
- I at position 34, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
- M at position 45, E at position 64, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69 and S at position 102 in the VL region sequence;
- S at position 30, M at position 45, A at position 65, G at position 68, V at position 81, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, S at position 69 and Y at position 93 in the VL region sequence; and
- S at position 30, M at position 45, E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, K at position 40 and S at position 69 in the VL region sequence;
- ii. E at position 64, A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;
- A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, S at position 106 in the VH region sequence, I at position 20, S

- at position 69 and S at position 102 in the VL region sequence;
 I at position 34, A at position 65, A at position 99, A at position 101, T at position 106
 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in
 the VL region sequence; and
- 5 S at position 30, E at position 39, E at position 64, A at position 65, V at position 81, A
 at position 101, E at position 102, I at position 104, T at position 106 in the VH region
 sequence, M at position 20, K at position 40 and E at position 69 in the VL region
 sequence;
- iii. A at position 101 in the VH region sequence;
- 10 iv. V at position 81, A at position 99 in the VH region sequence, I at position 20, K at
 position 40, S at position 69 and S at position 102 in the VL region sequence;
 I at position 34, V at position 81 in the VH region sequence, I at position 20, K at
 position 40 and S at position 102 in the VL region sequence;
 I at position 34 in the VH region sequence, I at position 20, K at position 40 and S at
 15 position 102 in the VL region sequence;
 I at position 34, E at position 39, V at position 81 in the VH region sequence, I at
 position 20, K at position 40 and S at position 102 in the VL region sequence;
- v. I at position 34, V at position 81 in the VH region sequence, and K at position
 40 in the VL region sequence;
- 20 M at position 45 in the VH region sequence, I at position 20, K at position 40 and S
 at position 102 in the VH region sequence;
 I at position 34, A at position 65, A at position 101 and S at position 106 in the VH
 region sequence;
 I at position 20, K at position 40, S at position 69 and S at position 102 in the VL
 25 region sequence;
 F at position 34 and V at position 81 in the VH region sequence;
 M at position 45 in the VH region sequence, K at position 40 and S at position 102 in
 the VL region sequence;
- 30 D at position 39 in the VH region sequence, I at position 20, K at position 40 and S at
 position 102 in the VL region sequence;
 I at position 34 and V at position 81 in the VH region sequence;
 E at position 39 in the VH region sequence, I at position 20, K at position 40 and S
 at position 102 in the VL region sequence;
- 35 M at position 45 in the VH region sequence and K at position 40 in the VL region
 sequence;
 I at position 34, A at position 65, V at position 81, A at position 99, A at position
 101 and S at position 106 in the VH region sequence; or

- vi. D at position 39 in the VH region sequence, _I at position 20, _R at position 40 and _S at position 102 in the VL region sequence;
 I at position 34 in the VH region sequence;
 K at position 40 in the VL region sequence;
- 5 D at position 39_in the VH region sequence, K at position 40 and _S at position 102 in the VL region sequence;
 I at position 20 and _S at position 102 in the VH region sequence;
 K at position 39 in the VH region sequence;
 E at position 39 in the VH region sequence, _K at position 40_and S at position 102 in the VL region sequence;
- 10 E at position 39 in the VH region sequence, _I at position 20, _R at position 40_and S at position 102 in the VL region sequence;
 D at position 39_in the VH region sequence, _R at position 40_and S at position 102 in the VL region sequence;
- 15 V at position 81 in the VH region sequence;
 D at position 39 in the VH region sequence and _K at position 40 in the VL region sequence;
 F at position 112 in the VH region sequence;
 F at position 112 in the VH region sequence and _I at position 38 in the VL region sequence;
- 20 E at position 39 in the VH region sequence and K at position 40 in the VL region sequence;
 V at position 34 in the VH region sequence.
- 25 The above recited amino acid residues are present at the given position(s) in the CD3epsilon binding domain according to the invention. In case one of the VH and/or VL region sequences that are to be changed (the VH region of i) and the VL region of ii)), i.e. the base VH and/or VL region sequence, already contain one of the above recited amino acid residues at a given position, it follows that these cannot be changed since the respective amino acid
- 30 residue is already present in the VH region and/or VL region of i) and/or ii).
 More preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 362 and 363, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855. Even more preferred is that the
- 35 CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 730 and 731, 1664 and 1665, and 1854 and 1855. In a yet even more preferred embodiment, the CD3epsilon

- binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 730 and 731, 1664 and 1665, and 1854 and 1855. Most preferred is that said CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) of SEQ ID NOs: 1854 and 1855, respectively.
- 5 As evident from the example section, the above recited amino acid residues at the given position(s) have a favorable effect on an increase of the temperature stability that is measured by the well know and also herein described method of DSF (Differential Scanning Fluorimetry; cf. e.g., Wen et al., "Nano differential scanning fluorimetry for comparability studies of therapeutic proteins", Analytical Biochemistry, Volume 593, 2020, 113581, ISSN 0003-2697; Dart, M. L., et al. (2018). "Homogeneous Assay for Target Engagement Utilizing Bioluminescent Thermal Shift". ACS medicinal chemistry letters, 9(6), 546–551) when introduced in the above recited VH and VL sequences of i) and ii). More specifically, the amino acid residues at the given positions recited in sections i. and iv. exhibit an increase in temperature stability of 6 °C or more as compared to the value measured for the unmodified sequence, i.e. the respective base VH and VL sequence. Section ii. and v. exhibit an increase in temperature stability of 3 °C or more as compared to the value measured for the unmodified sequence, i.e. the respective base VH and VL sequence, whereas sections iii. and vi. exhibit an increase in temperature stability of 1 °C or more as compared to the value measured for the unmodified sequence, i.e. the respective base VH and VL sequence.
- 15
- 20 Preferably, the amino acid residues at the given position(s) in section i. ii., iv., and/or v. are present in the CD3epsilon binding domain according to this embodiment. More preferred is that the amino acid residues at the given position(s) in section i. and/or iv. are present in the CD3epsilon binding domain according to the invention. This preference also applies to the preferred embodiments recited in the following. As outlined herein, it is also preferred that
- 25 the VH and VL region is linked by a linker, preferably a peptide linker most preferred a G₄S or a G₄Q linker, preferably said G₄S or a G₄Q linker is repeated three times, i.e. it is a (G₄S)₃ or a (G₄Q)₃ linker.

[155] According to the invention, it relates to a polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region, wherein

30

- a) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 1854 and the VL region comprises or consists of the sequence as defined in SEQ ID NO: 1855; and wherein the VH and/or VL region sequence comprise the amino acid substitution(s) selected from:
- 35
- i. M34I, S65A, A81V, V99A, H101A, N106S in the VH region sequence (resulting VH sequence as defined in SEQ ID NO: 2012), L20I, Q40K, L69S,

and G102S in the VL region sequence (resulting VL sequence as defined in SEQ ID NO: 2013);

L45M, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO: 2036), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 2037);

L45M, S65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 2028), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region sequence (SEQ ID NO: 2029);

M34I, Q39E, S65A, H101N, G102A, N106T, W112F in the VH region sequence (SEQ ID NO: 2044), Q40K and G102S in the VL region sequence (SEQ ID NO: 2045);

M34I, D64E, S65A, V99A, H101A, N106T in the VH region sequence (SEQ ID NO: 34), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 35);

M34I, S65A, A81V, V99A, H101A, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 90), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 91);

D64E, S65A, D68G, A81V, H101A, N106S in the VH region sequence (SEQ ID NO: 100), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 101);

M34I, D64E, S65A, H101A, N106T, W112F in the VH region sequence (SEQ ID NO: 58), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 59);

M34I, D64E, S65A, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 50), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 51);

M34I, D64E, S65A, A81V, V99A, H101A, N106S in the VH region sequence (SEQ ID NO: 98), L20I, Q40K, L69S, G102S and W93Y in the VL region sequence (SEQ ID NO: 99);

M34I, S65A, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 42), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 43);

L45M, D64E, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO: 116), L20I, V38I, Q40K, L69E and G102S in the VL region sequence (SEQ ID NO: 117);

N30S, L45M, S65A, D68G, A81V, H101A, N106T, W112F in the VH region sequence (SEQ ID NO: 82), Q40K, L69S and W93Y in the VL region sequence (SEQ ID NO: 83); and

- N30S, L45M, D64E, S65A, D68G, A81V, H101A, N106S in the VH region sequence (SEQ ID NO: 74), Q40K and L69S in the VL region sequence (SEQ ID NO: 75);
- 5 ii. D64E, S65A, D68G, A81V, H101N, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 2020), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 2021);
- S65A, D68G, A81V, H101N, G102E, F104I, N106S in the VH region sequence (SEQ ID NO: 108), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 109);
- 10 M34I, S65A, V99A, H101A, N106T in the VH region sequence (SEQ ID NO: 26), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 27);
- and
- N30S, Q39E, D64E, S65A, A81V, H101A, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 66), L20M, Q40K and L69E in the VL region sequence (SEQ ID NO: 67);
- 15 iii. H101A in the VH region sequence (SEQ ID NO: 2560);
- iv. A81V, V99A_ in the VH region sequence, L20I, Q40K, L69S and G102S in the VL region sequence;
- M34I,_A81V in the VH region sequence (SEQ ID NO: 1898),_L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 1899);
- 20 M34I in the VH region sequence (SEQ ID NO: 1904), L20I,_Q40K_and G102S in the VL region sequence (1905);
- M34I,_Q39E,_A81V in the VH region sequence (SEQ ID NO: 1906), L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 1907);
- 25 v. M34I,_A81V in the VH region sequence (SEQ ID NO: 1900), and Q40K in the VL region sequence (SEQ ID NO: 1901);
- L45M in the VH region sequence (SEQ ID NO: 1866),_L20I,_Q40K and_G102S in the VH region sequence (SEQ ID NO: 1867);
- M34I,_S65A,_H101A and_N106S in the VH region sequence;
- 30 L20I,_Q40K,_L69S and_G102S in the VL region sequence;
- M34F_and A81V in the VH region sequence (SEQ ID NO: 1884);
- L45M in the VH region sequence (SEQ ID NO: 1870), Q40K and_G102S in the VL region sequence (SEQ ID NO: 1871);
- 35 Q39D in the VH region sequence (SEQ ID NO: 1918), L20I,_Q40K and G102S in the VL region sequence (SEQ ID NO: 1919);
- M34I_and A81V in the VH region sequence (SEQ ID NO: 1869);
- Q39E in the VH region sequence (SEQ ID NO:_1932), L20I,_Q40K

- and_G102S in the VL region sequence (SEQ ID NO: 1933);
 L45M in the VH region sequence (SEQ ID NO: 1868) and_Q40K in the VL
 region sequence (SEQ ID NO: 1869);
 M34I, S65A, A81V, V99A, H101A and N106S in the VH region sequence;
 5 or
- vi. Q39D in the VH region sequence (SEQ ID NO: 1928), L20I, Q40R
 and_G102S in the VL region sequence (SEQ ID NO: 1929);
 M34I in the VH region sequence (SEQ ID NO: 1892);
 Q40K in the VL region sequence (SEQ ID NO: 1974);
 10 Q39D in the VH region sequence (SEQ ID NO: 1922), Q40K and_G102S in
 the VL region sequence (SEQ ID NO: 1923);
 L20I and_G102S in the VH region sequence;
 Q39K in the VH region sequence (SEQ ID NO: 1944);
 Q39E in the VH regions sequence (SEQ ID NO: 1938), Q40K and G102S in
 15 the VL region sequence (SEQ ID NO: 1939);
 Q39E in the VH region sequence (SEQ ID NO: 1934), L20I, Q40R and
 G102S in the VL region sequence (SEQ ID NO: 1935);
 Q39D in the VH region sequence (SEQ ID NO: 1926), Q40R and G102S in
 the VL region sequence (SEQ ID NO: 1926);
 20 A81V in the VH region sequence (SEQ ID NO: 1862);
 Q39D in the VH region sequence (SEQ ID NO: 1920) and_Q40K in the VL
 region sequence (SEQ ID NO: 1921);
 W112F in the VH region sequence (SEQ ID NO: 1958);
 W112F in the VH region sequence (SEQ ID NO: 1960) and_V38I in the VL
 25 region sequence (SEQ ID NO: 1961);
 Q39E in the VH region sequence (SEQ ID NO: 1936) and_Q40K in the VL
 region sequence (SEQ ID NO: 1937);
 M34V in the VH region sequence (SEQ ID NO: 1914);
- b) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 730
 30 and the VL region comprises or consists of the sequence as defined in SEQ ID NO:
 731; and wherein the VH and/or VL region sequence comprise the amino acid
 substitution(s) selected from:
- i. M34I, S65A, A81V, V99A, H101A, N106S in the VH region sequence
 (resulting VH sequence as defined in SEQ ID NO: 846), L20I, Q40K, L69S,
 35 and G102S in the VL region sequence (resulting VL sequence as defined in
 SEQ ID NO: 847);
 L45M, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO:

- 870), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 871);
- L45M, S65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 862), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region sequence (SEQ ID NO: 863);
- M34I, Q39E, S65A, H101N, G102A, N106T, W112F in the VH region sequence (SEQ ID NO: 878), Q40K and G102S in the VL region sequence (SEQ ID NO: 879);
- M34I, D64E, S65A, V99A, H101A, N106T in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- M34I, S65A, A81V, V99A, H101A, G102E, F104I, N106T in the VH region sequence, L20I, Q40K, L69S, and G102S in the VL region sequence;
- D64E, S65A, A81V, H101A, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
- M34I, D64E, S65A, H101A, N106T, W112F in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- M34I, D64E, S65A, H101A, N106S, W112F in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- M34I, D64E, S65A, A81V, V99A, H101A, N106S in the VH region sequence, L20I, Q40K, L69S, G102S and W93Y in the VL region sequence;
- M34I, S65A, H101A, N106S, W112F in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- L45M, D64E, S65A, A81L, H101A, N106T in the VH region sequence, L20I, V38I, Q40K, L69E and G102S in the VL region sequence;
- N30S, L45M, S65A, A81V, H101A, N106T, W112F in the VH region sequence, Q40K, L69S and W93Y in the VL region sequence; and
- N30S, L45M, D64E, S65A, A81V, H101A, N106S in the VH region sequence, Q40K and L69S in the VL region sequence;
- ii. D64E, S65A, A81V, H101N, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 854), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 855);
- S65A, A81V, H101N, G102E, F104I, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
- M34I, S65A, V99A, H101A, N106T in the VH region sequence, Q40K, V91A and G102S in the VL region sequence; and
- N30S, Q39E, D64E, S65A, A81V, H101A, G102E, F104I, N106T in the VH region sequence, L20M, Q40K and L69E in the VL region sequence;

- iii. H101A in the VH region sequence;
- iv. A81V, V99A_in the VH region sequence, L20I, Q40K, L69S and G102S in the VL region sequence;
 M34I,_A81V in the VH region sequence (SEQ ID NO: 774),_L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 775);
 M34I in the VH region sequence (SEQ ID NO: 780), L20I,_Q40K_and G102S in the VL region sequence (781);
 M34I,_Q39E,_A81V in the VH region sequence (SEQ ID NO: 782), L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 783);
- 10 v. M34I,_A81V in the VH region sequence (SEQ ID NO: 776), and Q40K in the VL region sequence (SEQ ID NO: 777);
 L45M in the VH region sequence (SEQ ID NO: 742),_L20I,_Q40K and_G102S in the VH region sequence (SEQ ID NO: 743);
 M34I,_S65A,_H101A and_N106S in the VH region sequence;
 15 L20I,_Q40K,_L69S and_G102S in the VL region sequence;
 M34F_and A81V in the VH region sequence (SEQ ID NO: 760);
 L45M in the VH region sequence (SEQ ID NO: 746), Q40K and_G102S in the VL region sequence (SEQ ID NO: 747);
 Q39D in the VH region sequence (SEQ ID NO: 794), L20I,_Q40K and G102S in the VL region sequence (SEQ ID NO: 795);
 20 M34I_and A81V in the VH region sequence (SEQ ID NO: 772);
 Q39E in the VH region sequence (SEQ ID NO:_808), L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 809);
 L45M in the VH region sequence (SEQ ID NO:_744)_and_Q40K in the VI region sequence (SEQ ID NO: 745);
 25 M34I,_S65A,_A81V,_V99A,_H101A_and N106S in the VH region sequence;
 or
- vi. Q39D in the VH region sequence (SEQ ID NO: 796),_L20I,_Q40R and_G102S in the VL region sequence (SEQ ID NO: 797);
 30 M34I in the VH region sequence (SEQ ID NO: 768);
 Q40K in the VL region sequence (SEQ ID NO: 891);
 Q39D_in the VH region sequence (SEQ ID NO: 800), Q40K and_G102S in the VL region sequence (SEQ ID NO: 801);
 L20I and_G102S in the VH region sequence;
 35 Q39K in the VH region sequence (SEQ ID NO: 820);
 Q39E in the VH region sequence (SEQ ID NO: 814),_Q40K_and G102S in the VL region sequence (SEQ ID NO: 815);

- Q39E in the VH region sequence (SEQ ID NO: 810),_L20I,_Q40R_and G102S in the VL region sequence (SEQ ID NO: 811);
 Q39D_in the VH region sequence (SEQ ID NO: 804),_Q40R_and G102S in the VL region sequence (SEQ ID NO: 805);
 5 A81V in the VH region sequence (SEQ ID NO: 738);
 Q39D in the VH region sequence (SEQ ID NO: 798) and_Q40K in the VL region sequence (SEQ ID NO: 799);
 W112F in the VH region sequence (SEQ ID NO: 834);
 W112F in the VH region sequence (SEQ ID NO: 836) and_V38I in the VL region sequence (SEQ ID NO: 837);
 10 Q39E in the VH region sequence (SEQ ID NO: 812)_and_Q40K in the VL region sequence (SEQ ID NO: 813);
 M34V in the VH region sequence (SEQ ID NO: 790)
- c) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 1664
 15 and the VL region comprises or consists of the sequence as defined in SEQ ID NO: 1665; and wherein the VH and/or VL region sequence comprise the amino acid substitution(s) selected from:
- i. M34I, S65A, A81V, V99A, H101A, N106S in the VH region sequence (resulting VH sequence as defined in SEQ ID NO: 1780), L20I, Q40K, L69S, and G102S in the VL region sequence (resulting VL sequence as defined in SEQ ID NO: 1781);
 20 L45M, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO: 1804), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 1805);
 25 L45M, S65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 1796), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region sequence (SEQ ID NO: 1797);
 M34I, Q39E, S65A, H101N, G102A, N106T, W112F in the VH region sequence (SEQ ID NO: 1812), Q40K and G102S in the VL region sequence (SEQ ID NO: 1813);
 30 M34I, D64E, S65A, V99A, H101A, N106T in the VH region sequence, Q40K and G102S in the VL region sequence;
 M34I, S65A, A81V, V99A, H101A, G102E, F104I, N106T in the VH region sequence, L20I, Q40K, L69S, and G102S in the VL region sequence;
 35 D64E, S65A, D68G, A81V, H101A, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
 M34I, D64E, S65A, H101A, N106T, W112F in the VH region sequence, Q40K

- and G102S in the VL region sequence;
M34I, D64E, S65A, H101A, N106S, W112F in the VH region sequence, Q40K
and G102S in the VL region sequence;
M34I, D64E, S65A, A81V, V99A, H101A, N106S in the VH region sequence,
5 L20I, Q40K, L69S, G102S and W93Y in the VL region sequence;
M34I, S65A, H101A, N106S, W112F in the VH region sequence, Q40K and
G102S in the VL region sequence;
L45M, D64E, S65A, A81L, H101A, N106T in the VH region sequence, L20I,
V38I, Q40K, L69E and G102S in the VL region sequence;
10 N30S, L45M, S65A, D68G, A81V, H101A, N106T, W112F in the VH region
sequence, Q40K, L69S and W93Y in the VL region sequence; and
N30S, L45M, D64E, S65A, D68G, A81V, H101A, N106S in the VH region
sequence, Q40K and L69S in the VL region sequence;
ii. D64E, S65A, D68G, A81V, H101N, G102E, F104I, N106T in the VH region
15 sequence (SEQ ID NO: 1788), L20I, L69S, and G102S in the VL region
sequence (SEQ ID NO: 1789);
S65A, D68G, A81V, H101N, G102E, F104I, N106S in the VH region
sequence, L20I, L69S, and G102S in the VL region sequence;
M34I, S65A, V99A, H101A, N106T in the VH region sequence, Q40K and
20 G102S in the VL region sequence; and
N30S, Q39E, D64E, S65A, A81V, H101A, G102E, F104I, N106T in the VH
region sequence, L20M, Q40K and L69E in the VL region sequence;
iii. H101A in the VH region sequence;
iv. A81V, V99A_ in the VH region sequence, L20I, Q40K, L69S and G102S in the
25 VL region sequence;
M34I,_A81V in the VH region sequence (SEQ ID NO: 1708),_L20I,_Q40K
and _G102S in the VL region sequence (SEQ ID NO: 1709);
M34I in the VH region sequence (SEQ ID NO: 1714), L20I,_Q40K_and
G102S in the VL region sequence (1715);
30 M34I,_Q39E,_A81V in the VH region sequence (SEQ ID NO: 1716),
L20I,_Q40K and _G102S in the VL region sequence (SEQ ID NO: 1717);
v. M34I,_A81V in the VH region sequence (SEQ ID NO: 1710), and Q40K in the
VL region sequence (SEQ ID NO: 1711);
L45M in the VH region sequence (SEQ ID NO: 1676),_L20I,_Q40K
35 and _G102S in the VH region sequence (SEQ ID NO: 1677);
M34I,_S65A,_H101A and _N106S in the VH region sequence;
L20I,_Q40K,_L69S and _G102S in the VL region sequence;

- 5 M34F_and A81V in the VH region sequence (SEQ ID NO: 1694);
 L45M in the VH region sequence (SEQ ID NO: 1680), Q40K and_G102S in
 the VL region sequence (SEQ ID NO: 1681);
 Q39D in the VH region sequence (SEQ ID NO: 1728), L20I,_Q40K and
 G102S in the VL region sequence (SEQ ID NO: 1729);
 M34I_and A81V in the VH region sequence (SEQ ID NO: 1706);
 Q39E in the VH region sequence (SEQ ID NO:_1742), L20I,_Q40K
 and_G102S in the VL region sequence (SEQ ID NO: 1743);
 L45M in the VH region sequence (SEQ ID NO:_1678)_and_Q40K in the VI
 10 region sequence (SEQ ID NO: 1679);
 M34I,_S65A,_A81V,_V99A,_H101A_and N106S in the VH region sequence;
 or
 vi. Q39D in the VH region sequence (SEQ ID NO: 1730),_L20I,_Q40R
 and_G102S in the VL region sequence (SEQ ID NO: 1731);
 15 M34I in the VH region sequence (SEQ ID NO: 1702);
 Q40K in the VL region sequence (SEQ ID NO: 1755);
 Q39D_in the VH region sequence (SEQ ID NO: 1734), Q40K and_G102S in
 the VL region sequence (SEQ ID NO: 1735);
 L20I and_G102S in the VH region sequence;
 20 Q39K in the VH region sequence (SEQ ID NO: 1754);
 Q39E in the VH regions sequence (SEQ ID NO: 1748),_Q40K_and G102S in
 the VL region sequence (SEQ ID NO: 1749);
 Q39E in the VH region sequence (SEQ ID NO: 1744),_L20I,_Q40R_and
 G102S in the VL region sequence (SEQ ID NO: 1745);
 25 Q39D_in the VH region sequence (SEQ ID NO: 1738),_Q40R_and G102S in
 the VL region sequence (SEQ ID NO: 1739);
 A81V in the VH region sequence (SEQ ID NO: 1672);
 Q39D in the VH region sequence (SEQ ID NO: 1732) and_Q40K in the VL
 region sequence (SEQ ID NO: 1733);
 30 W112F in the VH region sequence (SEQ ID NO: 1768);
 W112F in the VH region sequence (SEQ ID NO: 1770) and_V38I in the VL
 region sequence (SEQ ID NO: 1771);
 Q39E in the VH region sequence (SEQ ID NO: 1746)_and_Q40K in the VL
 region sequence (SEQ ID NO: 1747);
 35 M34V in the VH region sequence (SEQ ID NO: 1724); or
 d) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 124
 and the VL region comprises or consists of the sequence as defined in SEQ ID NO:

125; and wherein the VH and/or VL region sequence comprise the amino acid substitution(s) selected from:

- i. Q65A, A81V, V99A, H101A, N106S in the VH region sequence (resulting VH sequence as defined in SEQ ID NO: 132), L20I, Q40K, L69S, and G102S in the VL region sequence (resulting VL sequence as defined in SEQ ID NO: 133);
L45M, Q65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO: 156), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 157);
L45M, Q65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 148), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region sequence (SEQ ID NO: 149);
Q39E, Q65A, H101N, N106T, W112F in the VH region sequence (SEQ ID NO: 164), Q40K and G102S in the VL region sequence (SEQ ID NO: 165);
D64E, Q65A, V99A, H101A, N106T in the VH region sequence, Q40K, T91A and G102S in the VL region sequence;
Q65A, A81V, V99A, H101A, A102E, F104I, N106T in the VH region sequence, L20I, Q40K, L69S, and G102S in the VL region sequence;
D64E, Q65A, D68G, A81V, H101A, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
D64E, Q65A, H101A, N106T, W112F in the VH region sequence, Q40K and G102S in the VL region sequence;
D64E, Q65A, H101A, N106S, W112F in the VH region sequence, Q40K and G102S in the VL region sequence;
D64E, Q65A, A81V, V99A, H101A, N106S in the VH region sequence, L20I, Q40K, L69S, G102S and W93Y in the VL region sequence;
Q65A, H101A, N106S, W112F in the VH region sequence, Q40K and G102S in the VL region sequence;
L45M, D64E, Q65A, A81L, H101A, N106T in the VH region sequence, L20I, V38I, Q40K, L69E and G102S in the VL region sequence;
N30S, L45M, Q65A, D68G, A81V, H101A, N106T, W112F in the VH region sequence, Q40K, L69S and W93Y in the VL region sequence; and
N30S, L45M, D64E, Q65A, D68G, A81V, H101A, N106S in the VH region sequence, Q40K and L69S in the VL region sequence;
- ii. D64E, Q65A, D68G, A81V, H101N, A102E, F104I, N106T in the VH region sequence (SEQ ID NO: 140), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 141);

- Q65A, D68G, A81V, H101N, A102E, F104I, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
 Q65A, V99A, H101A, N106T in the VH region sequence, Q40K and G102S in the VL region sequence; and
- 5 N30S, Q39E, D64E, Q65A, A81V, H101A, A102E, F104I, N106T in the VH region sequence, L20M, Q40K and L69E in the VL region sequence;
- iii. H101A in the VH region sequence;
- iv. A81V, V99A in the VH region sequence, L20I, Q40K, L69S and G102S in the VL region sequence;
- 10 A81V in the VH region sequence, L20I, Q40K and G102S in the VL region sequence;
 L20I, Q40K and G102S in the VL region sequence;
 Q39E, A81V in the VH region sequence, L20I, Q40K and G102S in the VL region sequence;
- 15 v. A81V in the VH region sequence, and Q40K in the VL region sequence;
 L45M in the VH region sequence, L20I, Q40K and G102S in the VH region sequence;
 Q65A, H101A and N106S in the VH region sequence;
 L20I, Q40K, L69S and G102S in the VL region sequence;
- 20 I34F and A81V in the VH region sequence;
 L45M in the VH region sequence, Q40K and G102S in the VL region sequence;
 Q39D in the VH region sequence, L20I, Q40K and G102S in the VL region sequence;
- 25 Q39E in the VH region sequence, L20I, Q40K and G102S in the VL region sequence;
 L45M in the VH region sequence and Q40K in the VL region sequence;
 Q65A, A81V, V99A, H101A and N106S in the VH region sequence; or
- vi. Q39D in the VH region sequence, L20I, Q40R and G102S in the VL region sequence;
- 30 Q40K in the VL region sequence;
 Q39D in the VH region sequence, Q40K and G102S in the VL region sequence;
 L20I and G102S in the VH region sequence;
- 35 Q39K in the VH region sequence;
 Q39E in the VH region sequence, Q40K and G102S in the VL region sequence;

Q39E in the VH region sequence, _L20I, _Q40R_ and G102S in the VL region sequence;

Q39D_in the VH region sequence, _Q40R_ and G102S in the VL region sequence);

5 A81V in the VH region sequence;

Q39D in the VH region sequence and _Q40K in the VL region sequence;

W112F in the VH region sequence;

W112F in the VH region sequence and _V38I in the VL region sequence;

Q39E in the VH region sequence_ and _Q40K in the VL region sequence;

10 M34V in the VH region sequence.

The alternatives a) to c) are preferred, more preferred is the alternative a) as recited above as CD3epsilon binding domain of the polypeptide or polypeptide construct of the invention. The above recited preferred linkers are also preferred for this embodiment, i.e (G₄S)₃ or G₄Q)₃.

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[156]

[157] In accordance with the invention, the polypeptide or polypeptide construct the invention may have linkers, half-life extending peptides, and other structural moieties as disclosed in SEQ ID NOs: 1 to 19 and 2551. Details on nature and functions of these structures are found in the sequence table disclosed herein.

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[158] The invention provides an embodiment wherein the polypeptide construct is in a format selected from the group consisting of scFv, and to the extent that a further binding domain is present (scFv)₂, diabodies and oligomers of any of the aforementioned formats. The term "is in a format" does not exclude that the construct can be further modified, e.g. by attachment or fusion to other moieties, as described herein. According to one embodiment of the polypeptide construct of the present invention, the domains comprising the herein described paratopes are in the format of an scFv. In an scFv, the VH region and the VL region are arranged in the order VH-VL or VL-VH (from N- to C-terminus). It is envisaged that the VH and the VL regions of the domain(s) are connected via a linker, preferably a peptide linker. In a preferred embodiment, the peptide linker is a G₄S, or G₄Q linker or repetitions thereof, such as preferably (G₄S)₃ (i.e. three repetitions of G₄S), or (G₄Q)₃ (i.e. three repetitions of G₄Q). According to one embodiment of the binding domain(s) comprising the herein described VH and the VL regions, the VH-region is positioned N-terminally of the linker, and the VL-region is positioned C-terminally of the linker. In other words, in one embodiment of the domains comprising the herein described paratopes, the scFv comprises from the N-terminus to the C-terminus: VH-linker-VL. It is furthermore envisaged that binding domain(s) (comprising the herein described paratopes) of the construct, in case the

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polypeptide or polypeptide construct comprises at least one further binding domain in addition to said CD3 epsilon binding domain, are connected via a linker, preferably a peptide linker. The construct may e.g. comprise the domains in the order (from N-terminus to C-terminus) CD3 binding domain – linker – further binding domain. The inverse order (further binding domain(s) – linker – CD3 binding domain) is also possible and is the preferred orientation.

[159] The linkers are preferably peptide linkers, more preferably short peptide linkers. In accordance with the present invention, a “peptide linker” comprises an amino acid sequence which connects the amino acid sequences of one domain with another (variable and/or binding) domain (e.g. a variable domain or a binding domain) of the construct. An essential technical feature of such peptide linker is that it does not comprise any polymerization activity. Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344. The peptide linkers can also be used to attach other domains or modules or regions (such as half-life extending domains) to the construct of the invention. Examples of useful peptide linkers are shown in SEQ ID NOs: 1 to 11 and 2551. In the present context, a “short” linker has between 2 and 50 amino acids, preferably between 3 and 35, between 4 and 30, between 5 and 25, between 6 and 20, or between 6 and 17 amino acids. The linker between two variable regions of one binding domain may have a different length (e.g. may be longer) than the linker between the two binding domains. For example, the linker between two variable regions of one binding domain may have a length between 7 and 15 amino acids, preferably between 9 and 13, and the linker between the two binding domains may have a length between 3 and 10 amino acids, preferably between 4 and 8. It is further envisaged that the peptide linkers are glycine/serine linkers, such as those depicted in SEQ ID NOs: 1 to 11 and 2551. Most of the amino acids in glycine/serine linkers are selected from glycine and serine.

[160] If a linker is used, this linker is preferably of a length and sequence to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities. For peptide linkers which connect the at least two binding domains (or the two variable regions forming one binding domain) in the construct, those peptide linkers are envisaged which comprise only a few amino acid residues, e.g. 12 amino acid residues or less. Thus, peptide linkers of 12, 11, 10, 9, 8, 7, 6 or 5 amino acid residues are preferred. An envisaged peptide linker with less than 5 amino acids comprises 4, 3, 2 or one amino acid(s), wherein Gly-rich linkers are preferred. A “single amino acid” linker in the context of said “peptide linker” is Gly. Another embodiment of a peptide linker is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e. Gly₄Ser (SEQ ID NO: 15), or polymers thereof, i.e. (Gly₄Ser)_x, where x is an integer of 1 or greater (e.g. 2 or 3), for example SEQ ID NOs: 1 and 2. Preferred linkers are depicted in SEQ ID NOs: 2, 4, 5,

6, 8, 10, 11, and 2551. Another preferred linker comprises or consists of (Gly4Ser)₆. The characteristics of said peptide linkers are known in the art and are described e.g. in Dall'Acqua et al. (Biochem. (1998) 37, 9266-9273), Cheadle et al. (Mol Immunol (1992) 29, 21-30) and Raag and Whitlow (FASEB (1995) 9(1), 73-80). Peptide linkers which do not
5 promote any secondary structures are preferred. The linkage of said domains to each other can be provided, e.g., by genetic engineering. Methods for preparing fused and operatively linked bispecific single chain constructs and expressing them in mammalian cells or bacteria are well-known in the art (e.g. WO 99/54440 or Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York,
10 2001). More preferred, said peptide linker is a G₄S, or G₄Q linker or repetitions thereof, such as (G₄S)₃ or (G₄Q)₃.

[161] According to one embodiment of the invention, the polypeptide construct of the invention is a "single chain construct" or "single chain polypeptide". In the case of a further binding domain, it is also envisaged that either the CD3 binding or the further (also termed
15 "second") or both binding domains may be in the format of a "single chain Fv" (scFv). Although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by an artificial linker – as described hereinbefore – that enables them to be made as a single protein chain in which the VL and VH regions pair to form a monovalent molecule; see e.g., Huston et al. (1988) Proc. Natl.
20 Acad. Sci USA 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are full-length antibodies or IgGs. A single-chain variable fragment (scFv) is hence a fusion protein of the variable region of the heavy chain (VH) and of the light chain (VL) of immunoglobulins, usually connected with a short linker peptide. The linker is
25 usually rich in glycine for flexibility, as well as serine or also threonine for solubility, and can either connect the N-terminus of the VH with the C-terminus of the VL, or vice versa. This protein retains the specificity of the original immunoglobulin, despite removal of the constant regions and introduction of the linker.

[162] Bispecific single chain molecules are known in the art and are described in
30 WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl, Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56. Techniques described for producing single chain constructs (see, inter alia, US Patent 4,946,778, Kontermann and Dübel (2010), loc. cit. and Little (2009), loc. cit.) can be
35 adapted to produce single chain constructs selectively and, preferably, specifically recognizing (an) elected target(s).

- [163] Bivalent (also called divalent) or bispecific single-chain variable fragments (bi-scFvs or di-scFvs) having the format (scFv)₂ can be engineered by linking two scFv molecules (e.g. with linkers as described hereinbefore). The linking can be done by producing a single polypeptide chain with two VH regions and two VL regions, yielding tandem scFvs (see e.g. Kufer, P. et al., (2004) Trends in Biotechnology 22(5):238-244). Another possibility is the creation of scFv molecules with linker peptides that are too short for the two variable regions to fold together (e.g. about five amino acids), forcing the scFvs to dimerize. In this case, the VH and the VL of a binding domain (binding either to CD3epsilon or the further target antigen) are not directly connected via a peptide linker. Thus, the VH of the CD3 binding domain may e.g. be fused to the VL of the further target antigen binding domain via a peptide linker, and the VH of the further target antigen binding domain is fused to the VL of the CD3 binding domain via such peptide linker. This type is known as diabodies (see e.g. Hollinger, Philipp et al., (July 1993) Proceedings of the National Academy of Sciences of the United States of America 90 (14): 6444-8.).
- [164] In accordance with the invention, the polypeptide or polypeptide construct the invention comprises at least one further binding domain. In other words, the polypeptide or polypeptide construct comprises the CD3epsilon binding domain defined herein above and at least one further binding domain. Said further binding domain can be a further CD3 binding domain, preferably one as defined herein. As such, the polypeptide can comprise two of the same CD3 binding domains as defined herein. Alternatively or additionally (in a construct comprising at least three binding domains), the at least one further binding domain binds to a different target, such as a cell surface antigen.
- [165] Preferably, said at least one further binding domain binds to a cell surface antigen. The term "cell surface antigen" as used herein denotes a molecule, which is displayed on the surface of a cell. In most cases, this molecule will be located in or on the plasma membrane of the cell such that at least part of this molecule remains accessible from outside the cell in tertiary form. A non-limiting example of a cell surface molecule, which is located in the plasma membrane is a transmembrane protein comprising, in its tertiary conformation, regions of hydrophilicity and hydrophobicity. Here, at least one hydrophobic region allows the cell surface molecule to be embedded, or inserted in the hydrophobic plasma membrane of the cell while the hydrophilic regions extend on either side of the plasma membrane into the cytoplasm and extracellular space, respectively. It will be appreciated that an extracellular epitope refers to an epitope comprised by a portion of a protein that is disposed in the extracellular space, for example a portion of a cell surface molecule that extends into the extracellular space when that cell surface molecule is a native configuration disposed, embedded, or inserted in the plasma membrane. Non-limiting examples of cell surface molecules which are located on the plasma membrane are proteins which have been

modified at a cysteine residue to bear a palmitoyl group, proteins modified at a C-terminal cysteine residue to bear a farnesyl group or proteins which have been modified at the C-terminus to bear a glycosyl phosphatidyl inositol ("GPI") anchor.

5 [166] Said cell surface antigen is preferably a tumor antigen. The term "tumor antigen" as used herein may be understood as those antigens that are presented on tumor cells. These antigens can be presented on the cell surface with an extracellular part, which is often combined with a transmembrane and cytoplasmic part of the molecule. These antigens can sometimes be presented only by tumor cells and never by the normal ones. Tumor antigens can be exclusively expressed on tumor cells or might represent a tumor specific mutation
10 compared to normal cells. In this case, they are called tumor-specific antigens. More common are antigens that are presented by tumor cells and normal cells, and they are called tumor-associated antigens. These tumor-associated antigens can be overexpressed compared to normal cells or are accessible for antibody binding in tumor cells due to the less compact structure of the tumor tissue compared to normal tissue.

15 [167] In a preferred embodiment, the tumor antigen is selected from the group consisting of BCMA (B-cell maturation antigen), CD123 (interleukin-3 receptor alpha chain (IL-3R)), CD19 (B-lymphocyte antigen CD19), CD20 (B-lymphocyte antigen CD20), CD22 (cluster of differentiation-22), CD33 (Siglec-3), CD70 (Cluster of Differentiation 70), CDH19 (Cadherin 19), CDH3 (Cadherin 3), CLL1 (C-type lectin domain family 12 member A), CS1 (CCND3
20 subset 1), CLDN6 (Claudin-6), CLDN18.2 (Claudin 18.2), DLL3 (Delta-like ligand 3), EGFRvIII (Epidermal growth factor receptor vIII), FLT3 (fms like tyrosine kinase 3), MAGEB2 (Melanoma-associated antigen B2), MART1 (Melanoma Antigen Recognized By T-Cells 1), MSLN (Mesothelin), MUC17 (Mucin-17), PSMA (prostate-specific membrane antigen), and STEAP1 (Metalloreductase STEAP1). These tumor antigens are well known in the art due to
25 their expression on tumor cells.

[168] Preferred CDR sequences and VH/VL region sequences for BCMA binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a BCMA binding domain as further binding domain
30 (with and without half-life extending domain) are defined in SEQ ID NOs: 2072 to 2095.

[169] Preferred CDR sequences and VH/VL region sequences for CD123 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD123 binding domain as further binding domain
35 (with and without half-life extending domain) are defined in SEQ ID NOs: 2096 to 2110.

[170] Preferred CDR sequences and VH/VL region sequences for CD19 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and

bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD19 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2111 to 2125.

[171] Preferred CDR sequences and VH/VL region sequences for CD20 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD20 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2126 to 2140.

[172] Preferred CDR sequences and VH/VL region sequences for CD22 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD22 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2141 to 2154.

[173] Preferred CDR sequences and VH/VL region sequences for CD33 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD33 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2155 to 2178.

[174] Preferred CDR sequences and VH/VL region sequences for CD70 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD70 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2179 to 2192.

[175] Preferred CDR sequences and VH/VL region sequences for CDH19 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CDH19 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2193 to 2212.

[176] Preferred CDR sequences and VH/VL region sequences for CDH3 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CDH3 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2213 to 2256.

[177] Preferred CDR sequences and VH/VL region sequences for CLL1 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CLL1 binding domain as further binding domain (with

and without half-life extending domain) are defined in SEQ ID NOs: 2257 to 2271.

5 **[178]** Preferred CDR sequences and VH/VL region sequences for CS1 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CS1 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2272 to 2285.

10 **[179]** Preferred CDR sequences and VH/VL region sequences for CLDN6 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CLDN6 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2286 to 2299.

15 **[180]** Preferred CDR sequences and VH/VL region sequences for CLDN18.2 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CLDN18.2 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2300 to 2314.

20 **[181]** Preferred CDR sequences and VH/VL region sequences for DLL3 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a DLL3 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2315 to 2328.

25 **[182]** Preferred CDR sequences and VH/VL region sequences for EGFRvIII binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a EGFRvIII binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2329 to 2342.

30 **[183]** Preferred CDR sequences and VH/VL region sequences for FLT3 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a FLT3 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2343 to 2357.

35 **[184]** Preferred CDR sequences and VH/VL region sequences for MAGEB2 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a MAGEB2 binding domain as further

binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2358 to 2378.

[185] Preferred CDR sequences and VH/VL region sequences for MART1 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention are defined in SEQ ID NOs: 2379 to 2387.

[186] Preferred CDR sequences and VH/VL region sequences for MSLN binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a MSLN binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2388 to 2431.

[187] Preferred CDR sequences and VH/VL region sequences for MUC17 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a MUC17 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2432 to 2445.

[188] Preferred CDR sequences and VH/VL region sequences for PSMA binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a PSMA binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2446 to 2475.

[189] Preferred bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having CD20 and CD22 binding domains as further binding domains (with and without a further CD3 binding domain as defined herein) and a half-life extending domain are defined in SEQ ID NOs: 2505 to 2516.

[190] Preferred bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having CS1 and BCMA binding domains as further binding domains and a half-life extending domain are defined in SEQ ID NOs: 2517 to 2522.

[191] Preferred bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having MSLN and CDH3 binding domains as further binding domains and a half-life extending domain are defined in SEQ ID NOs: 2529 to 2536.

[192] As laid out herein above, the polypeptide construct of the invention comprises a binding domain which binds to CD3 on the surface of a T cell. "CD3" (cluster of differentiation 3) is a T cell co-receptor composed of four chains. In mammals, the CD3 protein complex contains a CD3 γ (gamma) chain, a CD3 δ (delta) chain, and two CD3 ϵ (epsilon) chains. These four chains associate with the T cell receptor (TCR) and the so-called ζ (zeta) chain to form the "T cell receptor complex" and to generate an activation signal

in T lymphocytes. The CD3 γ (gamma), CD3 δ (delta), and CD3 ϵ (epsilon) chains are highly related cell-surface proteins of the immunoglobulin superfamily and each contain a single extracellular immunoglobulin domain. The intracellular tails of the CD3 molecules contain a single conserved motif known as an immunoreceptor tyrosine-based activation motif (ITAM), which is essential for the signaling capacity of the TCR. The CD3 epsilon molecule is a polypeptide which in humans is encoded by the CD3 epsilon gene which resides on chromosome 11. In the context of the present invention, CD3 is understood as a protein complex and T cell co-receptor that is involved in activating both the cytotoxic T cell (CD8+ naive T cells) and T helper cells (CD4+ naive T cells). It is typically composed of four distinct chains. Especially in mammals, the complex contains a CD3 γ chain, a CD3 δ chain, and two CD3 ϵ chains. These chains associate with the T-cell receptor (TCR) and the ζ -chain (zeta-chain) to generate an activation signal in T lymphocytes. The TCR, ζ -chain, and CD3 molecules together constitute the TCR complex.

[193] The redirected lysis of target cells via the recruitment of T cells by a construct which binds to CD3 on the T cell and to a target protein on the target cell generally involves cytolytic synapse formation and delivery of perforin and granzymes. The engaged T cells are capable of serial target cell lysis and are not affected by immune escape mechanisms interfering with peptide antigen processing and presentation, or clonal T cell differentiation; see e.g. WO 2007/042261.

[194] Cytotoxicity mediated by given tumor antigenxCD3 constructs can be measured in various ways. The "half maximal effective concentration" (EC50) is commonly used as a measure of potency of a biologically active molecule such as a construct of the present invention. It may be expressed in molar units. In the present case of measuring cytotoxicity, the EC50 value refers to the concentration of a construct inducing a cytotoxic response (lysis of target cells) halfway between the baseline and the maximum. Effector cells in a cytotoxicity assay can e.g. be stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). An EC50 value may typically be expected to be lower when stimulated / enriched CD8+ T cells are used as effector cells, compared with unstimulated PBMC. If the target cells are of macaque origin or express or are transfected with a given macaque tumor antigen, the effector cells should also be of macaque origin, such as a macaque T cell line, e.g. 4119LnPx. The target cells should express said tumor antigen on the cell surface. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with said tumor antigen. Alternatively, the target cells can be a tumor antigen positive natural expresser cell line, such as the human cancer lines. Usually EC50 values are expected to be lower when using target cells that express higher levels of said tumor antigen on the cell surface compared with target cells having a lower target expression rate.

[195] The effector to target cell (E:T) ratio in a cytotoxicity assay is usually about 10:1, but can also vary. Cytotoxic activity of tumor antigenxCD3 constructs can be measured in a 51-chromium release assay (e.g. with an incubation time of about 18 hours) or in a FACS-based cytotoxicity assay (e.g. with an incubation time of about 48 hours). Modifications of the incubation time (cytotoxic reaction) are also envisaged. Other methods of measuring cytotoxicity are well-known and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

[196] According to one embodiment, the cytotoxic activity mediated by tumor antigenxCD3 constructs of the present invention is measured in a cell-based cytotoxicity assay. It may also be measured in a 51-chromium release assay. It is envisaged that the EC₅₀ value of the constructs of the invention is ≤ 300 pM, ≤ 280 pM, ≤ 260 pM, ≤ 250 pM, ≤ 240 pM, ≤ 220 pM, ≤ 200 pM, ≤ 180 pM, ≤ 160 pM, ≤ 150 pM, ≤ 140 pM, ≤ 120 pM, ≤ 100 pM, ≤ 90 pM, ≤ 80 pM, ≤ 70 pM, ≤ 60 pM, ≤ 50 pM, ≤ 40 pM, ≤ 30 pM, ≤ 20 pM, ≤ 15 pM, ≤ 10 pM, or ≤ 5 pM.

[197] The above given EC₅₀ values can be measured in different assays and under different conditions. For example, when human PBMCs are used as effector cells and tumor antigen transfected cells such as CHO cells are used as target cells, it is envisaged that the EC₅₀ value of the tumor antigenxCD3 construct is ≤ 500 pM, ≤ 400 pM, ≤ 300 pM, ≤ 280 pM, ≤ 260 pM, ≤ 250 pM, ≤ 240 pM, ≤ 220 pM, ≤ 200 pM, ≤ 180 pM, ≤ 160 pM, ≤ 150 pM, ≤ 140 pM, ≤ 120 pM, ≤ 100 pM, ≤ 90 pM, ≤ 80 pM, ≤ 70 pM, ≤ 60 pM, ≤ 50 pM, ≤ 40 pM, ≤ 30 pM, ≤ 20 pM, ≤ 15 pM, ≤ 10 pM, or ≤ 5 pM. When human PBMCs are used as effector cells and when the target cells are a CLDN6 positive cell line such as, it is envisaged that the EC₅₀ value of the CLDN6xCD3 construct is ≤ 300 pM, ≤ 280 pM, ≤ 260 pM, ≤ 250 pM, ≤ 240 pM, ≤ 220 pM, ≤ 200 pM, ≤ 180 pM, ≤ 160 pM, ≤ 150 pM, ≤ 140 pM, ≤ 120 pM, ≤ 100 pM, ≤ 90 pM, ≤ 80 pM, ≤ 70 pM, ≤ 60 pM, ≤ 50 pM, ≤ 40 pM, ≤ 30 pM, ≤ 20 pM, ≤ 15 pM, ≤ 10 pM, or ≤ 5 pM.

[198] According to one embodiment, the tumor antigenxCD3 polypeptides/polypeptide constructs of the present invention do not induce / mediate lysis or do not essentially induce / mediate lysis of cells that do not express said given tumor antigen on their surface (tumor antigen negative cells), such as CHO cells. The term “do not induce lysis”, “do not essentially induce lysis”, “do not mediate lysis” or “do not essentially mediate lysis” means that a construct of the present invention does not induce or mediate lysis of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% of tumor antigen negative cells, whereby lysis of tumor antigen expressing target cells (such as cells transformed or transfected with said tumor antigen or a natural expresser cell line such as the human cancer lines) is set to be 100%. This usually applies for concentrations of the construct of up to 500 nM. Cell lysis

measurement is a routine technique. Moreover, the present specification teaches specific instructions how to measure cell lysis.

[199] The difference in cytotoxic activity between the monomeric and the dimeric isoform of individual tumor antigenxCD3 polypeptides/polypeptide constructs is referred to as “potency gap”. This potency gap can e.g. be calculated as ratio between EC50 values of the molecule’s monomeric and dimeric form. In one method to determine this gap, an 18 hour 51-chromium release assay or a 48h FACS-based cytotoxicity assay is carried out as described hereinbelow with purified construct monomer and dimer. Effector cells are stimulated enriched human CD8+ T cells or unstimulated human PBMC. Target cells are hu tumor antigen transfected CHO cells. Effector to target cell (E:T) ratio is 10:1. Potency gaps of the tumor antigenxCD3 constructs of the present invention are preferably ≤ 5 , more preferably ≤ 4 , even more preferably ≤ 3 , even more preferably ≤ 2 and most preferably ≤ 1 .

[200] The binding domain(s) of the polypeptide construct of the invention is/are preferably cross-species specific for members of the mammalian order of primates, such as macaques. According to one embodiment, the further binding domain(s), in addition to binding to a human tumor antigen, will also bind to said tumor antigen of primates including (but not limited to) new world primates (such as *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus*), old world primates (such as baboons and macaques), gibbons, orangutans and non-human hominidae. It is envisaged that the domain which binds to human CD3 on the surface of a T cell of the invention also binds at least to macaque CD3. A preferred macaque is *Macaca fascicularis*. *Macaca mulatta* (Rhesus) is also envisaged. The polypeptide or polypeptide construct of the invention comprises a domain which binds to human CD3epsilon on the surface of a T cell and at least macaque CD3.

[201] In one embodiment, the affinity gap of the constructs according to the invention for binding macaque CD3 versus human CD3 [KD ma CD3 : KD hu CD3] (as determined e.g. by BiaCore or by Scatchard analysis) is between 0.01 and 100, preferably between 0.1 and 10, more preferably between 0.2 and 5, more preferably between 0.3 and 4, even more preferably between 0.5 and 3 or between 0.5 and 2.5, and most preferably between 0.5 and 1.

[202] As detailed herein above, said binding domain of the polypeptide or polypeptide construct of the invention binds to human CD3 epsilon (or human CD3 epsilon on the surface of a T cell) and, preferably, to *Callithrix jacchus* or *Saimiri sciureus* CD3 epsilon. More specifically, said domain binds to an extracellular epitope of human CD3 epsilon. It is also envisaged that said domain binds to an extracellular epitope of the human and the *Macaca* CD3 epsilon chain. Said extracellular epitope of CD3 epsilon is comprised within amino acid residues 1-27 of the human CD3 epsilon extracellular domain (see SEQ ID NO: 2552; amino

acid residues 1-27 in SEQ ID NO: 2553). Even more particularly, the epitope comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu. *Callithrix jacchus* is a new world primate belonging to the family of Callitrichidae, while *Saimiri sciureus* is a new world primate belonging to the family of Cebidae.

5 **[203]** In a preferred embodiment, the polypeptide or polypeptide construct of the invention is a single chain polypeptide that is at least bispecific. It is preferred for this embodiment that the CD3 binding domain according to the invention is present as a scFv in the polypeptide or polypeptide construct.

10 **[204]** It is also envisaged that the polypeptide construct of the invention has, in addition to its function to bind to CD3 and, in certain embodiments to bind to at least a further binding domain, a further function. In this format, the construct may be a trifunctional or multifunctional construct by targeting target cells through, preferably, tumor antigen binding, mediating cytotoxic T cell activity through CD3 binding and providing a further function such as means or domains to enhance or extend serum half-life, a fully functional or modified Fc
15 constant domain mediating cytotoxicity through recruitment of effector cells, a label (fluorescent etc.), a therapeutic agent such as a toxin or radionuclide, etc.

20 **[205]** Examples for means or domains to extend serum half-life of the polypeptides/polypeptide constructs of the invention include peptides, proteins or domains of proteins, which are fused or otherwise attached to the polypeptides/polypeptide constructs. The group of peptides, proteins or protein domains includes peptides binding to other proteins with preferred pharmacokinetic profile in the human body such as serum albumin (see WO 2009/127691). An alternative concept of such half-life extending peptides includes peptides binding to the neonatal Fc receptor (FcRn, see WO 2007/098420), which can also be used in the constructs of the present invention. The concept of attaching larger domains
25 of proteins or complete proteins includes the fusion of human serum albumin, variants or mutants of human serum albumin (see WO 2011/051489, WO 2012/059486, WO 2012/150319, WO 2013/135896, WO 2014/072481, WO 2013/075066) or domains thereof, as well as the fusion of an immunoglobulin constant region (Fc domain) and variants thereof. Such variants of Fc domains are called Fc-based domains and may e.g. be
30 optimized / modified to allow the desired pairing of dimers or multimers, to abolish Fc receptor binding (e.g. to avoid ADCC or CDC) or for other reasons. A further concept known in the art to extend the half-life of substances or molecules in the human body is the pegylation of those molecules (such as the constructs of the present invention).

35 **[206]** In one embodiment, the polypeptides/polypeptide constructs according to the invention are linked (e.g. via peptide bond) with a fusion partner (such as a protein, polypeptide or peptide), e.g. for extending the construct's serum half-life. These fusion

partners can be selected from human serum albumin ("HSA" or "HALB") as well as sequence variants thereof, peptides binding to HSA, peptides binding to FcRn ("FcRn BP"), or constructs comprising an (antibody derived) Fc region. Exemplary sequences of these fusion partners are depicted in SEQ ID NOs: 16, 18 and 19. In general, the fusion partners may be linked to the N-terminus or to the C-terminus of the constructs according to the invention, either directly (e.g. via peptide bond) or through a peptide linker such as (GGGGS)_n or (GGGGQ)_n (wherein "n" is an integer of 2 or greater, e.g. 2 or 3 or 4). Suitable peptide linkers are discussed above and are shown in SEQ ID NOs: 2 and 2551.

[207] It is envisaged that a polypeptide construct according to the present invention comprises a single chain polypeptide that is at least bispecific, wherein said polypeptide comprises or consists of in the following order from N-terminus to C-terminus:

- a) VL (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VH (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope);
- b) VH (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope);
- c) VL (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VH (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope) - Peptide linker (G4) - Fc monomer (part of the HLE domain) - (G4S)₆ or (G4Q)₆ or - Fc monomer (part of the HLE domain);
- d) VH (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope) - Peptide linker (G4) - Fc monomer (part of the HLE domain) - (G4S)₆ or (G4Q)₆ or - Fc monomer (part of the HLE domain);
- e) VH (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of a first cell surface antigen binding

domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VL (comprising part of a second cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VH (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain);

f) VH (comprising part of a first cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of a first cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of a second cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain);

g) VL (comprising part of a first cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VL (comprising part of a second cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VH (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain)

h) VL (comprising part of a first cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of a second cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain); or

i) **Binding domain 1** ((VL (comprising part of a first cell surface antigen binding domain/paratope) – (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen

binding domain/paratope)) or (VH (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VL (comprising part of a first cell surface antigen binding domain/paratope))) – **Peptide linker (G4S) or (G4Q) – CD3 binding domain 1** (VH (comprising part of a first CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of a first CD3epsilon binding domain/paratope)) – **Peptide linker (G4) – Fc monomer** (part of the HLE domain) – **(G4S)6 or (G4Q)6 – Fc monomer** (part of the HLE domain) – **Peptide linker (G4) – Binding domain 2** ((VL (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen binding domain/paratope)) or (VH (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VL (comprising part of a second cell surface antigen binding domain/paratope))) – **Peptide linker (G4S) or (G4Q) – CD3 binding domain 2** (VH (comprising part of a second CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of a second CD3epsilon binding domain/paratope))).

[208] As is evident from the above, the VH and VL region sequence orientation of the binding domain(s) of the cell surface antigen can be VH-VL or VL-VH. Preferably, the cell surface antigen is a tumor antigen as detailed herein above. The HLE domain sequences made up of the Fc monomers and connecting linkers as detailed are preferably selected from the sequences as defined in SEQ ID NOs: 18 and 19. The two CD3 binding domains of the polypeptide construct of item i) are preferably the same CD3 binding domains, such as, preferably, the CD3 binding domain with VH and VL region sequences of SEQ ID NOs: 2028 and 2029. While peptide linkers (SG4S) or (SG4Q) are preferred at the indicated positions, they can also be replaced by (G4S) or (G4Q) linkers.

[209] Covalent modifications of the polypeptides/polypeptide constructs are also included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the construct are introduced into the molecule by reacting specific amino acid residues of the construct with an organic derivatizing agent that can react with selected side chains or with the N- or C-terminal residues. Derivatization with bifunctional agents is useful for crosslinking the constructs of the present invention to a water-insoluble support matrix or surface for use in a variety of methods. Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention. Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and

Molecular Properties, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[210] Another type of covalent modification of the constructs included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of specific glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Specific expression systems are discussed below. Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[211] Addition of glycosylation sites to the construct is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the amino acid sequence of a construct may be altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[212] Another means of increasing the number of carbohydrate moieties on the construct is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330, and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306.

[213] Removal of carbohydrate moieties present on the starting construct may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This

treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin et al., 1987, Arch. Biochem. Biophys. 259:52 and by Edge et al., 1981, Anal. Biochem. 118:131. Enzymatic cleavage of carbohydrate
 5 moieties on polypeptides can be achieved using a variety of endo- and exo-glycosidases as described by Thotakura et al., 1987, Meth. Enzymol. 138:350. Glycosylation at potential glycosylation sites may be prevented using the compound tunicamycin as described by Duskin et al., 1982, J. Biol. Chem. 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

10 **[214]** Other modifications of the construct are also contemplated herein. For example, another type of covalent modification of the construct comprises linking the construct to various non-proteinaceous polymers, including polyols, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions
 15 within the construct, e.g. to facilitate the addition of polymers such as polyethylene glycol (PEG).

[215] In some embodiments, the covalent modification of the constructs of the invention comprises the addition of one or more labels. The labelling group may be coupled to the construct via spacer arms of various lengths to reduce potential steric hindrance. Various
 20 methods for labelling proteins are known in the art and can be used in performing the present invention. The term "label" or "labelling group" refers to any detectable label. In general, labels fall into a variety of classes, depending on the assay in which they are to be detected – the following examples include, but are not limited to:

- 25 a) isotopic labels, which may be radioactive or heavy isotopes, such as radioisotopes or radionuclides (e.g., ^3H , ^{14}C , ^{15}N , ^{35}S , ^{89}Zr , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I)
- b) magnetic labels (e.g., magnetic particles)
- c) redox active moieties
- d) optical dyes (including, but not limited to, chromophores, phosphors and fluorophores) such as fluorescent groups (e.g., FITC, rhodamine, lanthanide phosphors),
 30 chemiluminescent groups, and fluorescent labels or fluorophores which can be either "small molecule" fluoeres or proteinaceous fluoeres
- e) enzymatic groups (e.g. horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase)
- f) biotinylated groups
- 35 g) predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.).

[216] By "fluorescent label" is meant any molecule that may be detected via its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland.

[217] Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie et al., 1994, Science 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank® Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, Biotechniques 24:462-471; Heim et al., 1996, Curr. Biol. 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki et al., 1993, J. Immunol. 150:5408-5417), β galactosidase (Nolan et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5,292,658; 5,418,155; 5,683,888; 5,741,668; 5,777,079; 5,804,387; 5,874,304; 5,876,995; 5,925,558).

[218] Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., 1988, Science 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe et al., 1994, FEBS Letters 344:191. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow et al., 1994, Semin. Immunol. 6:267-78.

[219] The polypeptide construct of the invention may also comprise additional domains, which are e.g. helpful in the isolation of the molecule or relate to an adapted pharmacokinetic profile of the molecule. Domains helpful for the isolation of a construct may be selected from peptide motives or secondarily introduced moieties, which can be captured in an isolation

method, e.g. an isolation column. Non-limiting embodiments of such additional domains comprise peptide motives known as Myc-tag, HAT-tag, HA-tag, TAP-tag, GST-tag, chitin binding domain (CBD-tag), maltose binding protein (MBP-tag), Flag-tag, Strep-tag and variants thereof (e.g. StrepII-tag) and His-tag. All herein disclosed constructs characterized
5 by the identified CDRs may comprise a His-tag domain, which is generally known as a repeat of consecutive His residues in the amino acid sequence of a molecule, e.g. of five His residues, or of six His residues (hexa-histidine). The His-tag may be located e.g. at the N- or C-terminus of the construct. In one embodiment, a hexa-histidine tag (HHHHHH) is linked via peptide bond to the C-terminus of the construct according to the invention. A histidine tag is
10 preferred, especially a 6x His tag.

[220] The invention also relates to a polynucleotide encoding a polypeptide or polypeptide construct of the invention. Nucleic acid molecules are biopolymers composed of nucleotides. A polynucleotide is a biopolymer composed of 13 or more nucleotide monomers covalently bonded in a chain. DNA (such as cDNA) and RNA (such as mRNA) are examples of
15 polynucleotides / nucleic acid molecules with distinct biological function. Nucleotides are organic molecules that serve as the monomers or subunits of nucleic acid molecules like DNA or RNA. The nucleic acid molecule or polynucleotide of the present invention can be double stranded or single stranded, linear or circular. It is envisaged that the nucleic acid molecule or polynucleotide is comprised in a vector. It is furthermore envisaged that such
20 vector is comprised in a host cell. Said host cell is, e.g. after transformation or transfection with the vector or the polynucleotide / nucleic acid molecule of the invention, capable of expressing the construct. For this purpose, the polynucleotide or nucleic acid molecule is operatively linked with control sequences.

[221] The genetic code is the set of rules by which information encoded within genetic material (nucleic acids) is translated into proteins. Biological decoding in living cells is accomplished by the ribosome which links amino acids in an order specified by mRNA, using tRNA molecules to carry amino acids and to read the mRNA three nucleotides at a time. The code defines how sequences of these nucleotide triplets, called codons, specify which amino acid will be added next during protein synthesis. With some exceptions, a three-nucleotide
30 codon in a nucleic acid sequence specifies a single amino acid. Because the vast majority of genes are encoded with exactly the same code, this particular code is often referred to as the canonical or standard genetic code.

[222] Degeneracy of codons is the redundancy of the genetic code, exhibited as the multiplicity of three-base pair codon combinations that specify an amino acid. Degeneracy
35 results because there are more codons than encodable amino acids. The codons encoding one amino acid may differ in any of their three positions; however, often this difference is in

the second or third position. For instance, codons GAA and GAG both specify glutamic acid and exhibit redundancy; but, neither specifies any other amino acid nor thus demonstrate ambiguity. The genetic codes of different organisms can be biased towards using one of the several codons that encode the same amino acid over the others – that is, a greater
5 frequency of one will be found than expected by chance. For example, leucine is specified by six distinct codons, some of which are rarely used. Codon usage tables detailing genomic codon usage frequencies for most organisms are available. Recombinant gene technologies commonly take advantage of this effect by implementing a technique termed codon optimization, in which those codons are used to design a polynucleotide which are preferred
10 by the respective host cell (such as a cell of human hamster origin, an *Escherichia coli* cell, or a *Saccharomyces cerevisiae* cell), e.g. to increase protein expression. It is hence envisaged that the polynucleotides / nucleic acid molecules of the present disclosure are codon optimized. Nevertheless, the polynucleotide / nucleic acid molecule encoding a construct of the invention may be designed using any codon that encodes the desired amino
15 acid.

[223] According to one embodiment, the polynucleotide / nucleic acid molecule of the present invention encoding the polypeptide construct of the invention is in the form of one single molecule or in the form of two or more separate molecules. If the construct of the present invention is a single chain construct, the polynucleotide / nucleic acid molecule
20 encoding such construct will most likely also be in the form of one single molecule. However, it is also envisaged that different components of the polypeptide construct (such as the different domains, e.g. the paratope (antigen-binding (epitope-binding) structure)-comprising domain which binds to a cell surface antigen, the paratope (antigen-binding (epitope-binding) structure)-comprising domain which binds to CD3, and/or further domains such as antibody
25 constant domains) are located on separate polypeptide chains, in which case the polynucleotide / nucleic acid molecule is most likely in the form of two or more separate molecules.

[224] The same applies for the vector comprising a polynucleotide / nucleic acid molecule of the present invention. If the construct of the present invention is a single chain construct,
30 one vector may comprise the polynucleotide which encodes the construct in one single location (as one single open reading frame, ORF). One vector may also comprise two or more polynucleotides / nucleic acid molecules at separate locations (with individual ORFs), each one of them encoding a different component of the construct of the invention. It is envisaged that the vector comprising the polynucleotide / nucleic acid molecule of the
35 present invention is in the form of one single vector or two or more separate vectors. In one embodiment, and for the purpose of expressing the construct in a host cell, the host cell of the invention should comprise the polynucleotide / nucleic acid molecule encoding the

construct or the vector comprising such polynucleotide / nucleic acid molecule in their entirety, meaning that all components of the construct – whether encoded as one single molecule or in separate molecules / locations – will assemble after translation and form together the biologically active construct of the invention.

5 [225] The invention further relates to a vector comprising a polynucleotide / nucleic acid molecule of the invention. A vector is a nucleic acid molecule used as a vehicle to transfer (foreign) genetic material into a cell, usually to ensure the replication and/or expression of the genetic material. The term “vector” encompasses – but is not restricted to – plasmids, viruses, cosmids, and artificial chromosomes. Some vectors are designed specifically for
10 cloning (cloning vectors), others for protein expression (expression vectors). So-called transcription vectors are mainly used to amplify their insert. The manipulation of DNA is normally conducted on *E. coli* vectors, which contain elements necessary for their maintenance in *E. coli*. However, vectors may also have elements that allow them to be maintained in another organism such as yeast, plant or mammalian cells, and these vectors
15 are called shuttle vectors. Insertion of a vector into the target or host cell is usually called transformation for bacterial cells and transfection for eukaryotic cells, while insertion of a viral vector is often called transduction.

[226] In general, engineered vectors comprise an origin of replication, a multicloning site and a selectable marker. The vector itself is generally a nucleotide sequence, commonly a
20 DNA sequence, that comprises an insert (transgene) and a larger sequence that serves as the “backbone” of the vector. While the genetic code determines the polypeptide sequence for a given coding region, other genomic regions can influence when and where these polypeptides are produced. Modern vectors may therefore encompass additional features besides the transgene insert and a backbone: promoter, genetic marker, antibiotic
25 resistance, reporter gene, targeting sequence, protein purification tag. Vectors called expression vectors (expression constructs) specifically are for the expression of the transgene in the target cell, and generally have control sequences.

[227] The term “control sequences” refers to DNA sequences necessary for the expression of an operably linked coding sequence in a specific host organism. The control sequences
30 that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, a Kozak sequence and enhancers.

[228] A nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is
35 operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding

sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned to facilitate translation. Generally, "operably linked" means that the nucleotide sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be
5 contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[229] "Transfection" is the process of deliberately introducing nucleic acid molecules or polynucleotides (including vectors) into target cells. The term is mostly used for non-viral
10 methods in eukaryotic cells. Transduction is often used to describe virus-mediated transfer of nucleic acid molecules or polynucleotides. Transfection of animal cells typically involves opening transient pores or "holes" in the cell membrane, to allow the uptake of material. Transfection can be carried out using biological particles (such as viral transfection, also called viral transduction), chemical-based methods (such as using calcium phosphate,
15 lipofection, Eugene, cationic polymers, nanoparticles) or physical treatment (such as electroporation, microinjection, gene gun, cell squeezing, magnetofection, hydrostatic pressure, impalefection, sonication, optical transfection, heat shock).

[230] The term "transformation" is used to describe non-viral transfer of nucleic acid molecules or polynucleotides (including vectors) into bacteria, and into non-animal eukaryotic
20 cells, including plant cells. Transformation is hence the genetic alteration of a bacterial or non-animal eukaryotic cell resulting from the direct uptake through the cell membrane(s) from its surroundings and subsequent incorporation of exogenous genetic material (nucleic acid molecules). Transformation can be achieved by artificial means. For transformation to happen, cells or bacteria must be in a state of competence, which might occur as a time-
25 limited response to environmental conditions such as starvation and cell density and can also be artificially induced.

[231] Moreover, the invention provides a host cell transformed or transfected with the polynucleotide / nucleic acid molecule of the invention or with the vector of the invention.

[232] As used herein, the terms "host cell" or "recipient cell" are intended to include any
30 individual cell or cell culture that can be or has been recipient of vectors, exogenous nucleic acid molecules and/or polynucleotides encoding the construct of the present invention; and/or recipients of the construct itself. The introduction of the respective material into the cell is carried out by way of transformation, transfection and the like (vide supra). The term "host cell" is also intended to include progeny or potential progeny of a single cell. Because
35 certain modifications may occur in succeeding generations due to either natural, accidental, or deliberate mutation or due to environmental influences, such progeny may not, in fact, be

completely identical (in morphology or in genomic or total DNA complement) to the parent cell but is still included within the scope of the term as used herein. Suitable host cells include prokaryotic or eukaryotic cells and include – but are not limited to – bacteria (such as *E. coli*), yeast cells, fungi cells, plant cells, and animal cells such as insect cells and mammalian cells, e.g., hamster, murine, rat, macaque or human.

[233] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for the construct of the invention. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*, *Kluyveromyces* hosts such as *K. lactis*, *K. fragilis* (ATCC 12424), *K. bulgaricus* (ATCC 16045), *K. wickerhamii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilae* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402 226); *Pichia pastoris* (EP 183 070); *Candida*; *Trichoderma reesei* (EP 244 234); *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*.

[234] Suitable host cells for the expression of a glycosylated construct are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruit fly), and *Bombyx mori* (silkworm) have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

[235] Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, *Arabidopsis* and tobacco can also be used as hosts. Cloning and expression vectors useful in the production of proteins in plant cell culture are known to those of skill in the art. See e.g. Hiatt et al., *Nature* (1989) 342: 76-78, Owen et al. (1992) *Bio/Technology* 10: 790-794, Artsaenko et al. (1995) *The Plant J* 8: 745-750, and Fecker et al. (1996) *Plant Mol Biol* 32: 979-986.

[236] However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (cell culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (such as COS-7, ATCC CRL 1651); human embryonic kidney line (such as 293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen Virol.* 36: 59 (1977)); baby hamster kidney cells (such as BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (such as CHO, Urlaub et

al., Proc. Natl. Acad. Sci. USA 77: 4216 (1980)); mouse sertoli cells (such as TM4, Mather, Biol. Reprod. 23: 243-251 (1980)); monkey kidney cells (such as CV1 ATCC CCL 70); African green monkey kidney cells (such as VERO-76, ATCC CRL1587); human cervical carcinoma cells (such as HELA, ATCC CCL 2); canine kidney cells (such as MDCK, ATCC CCL 34);
5 buffalo rat liver cells (such as BRL 3A, ATCC CRL 1442); human lung cells (such as W138, ATCC CCL 75); human liver cells (such as Hep G2, 1413 8065); mouse mammary tumor (such as MMT 060562, ATCC CCL-51); TRI cells (Mather et al., Annals N. Y Acad. Sci. (1982) 383: 44-68); MRC 5 cells; FS4 cells; and a human hepatoma line (such as Hep G2).

[237] In a further embodiment, the invention provides a process for the production of a
10 polypeptide or polypeptide construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the construct of the invention and recovering the produced construct from the culture.

[238] As used herein, the term "culturing" refers to the in vitro maintenance, differentiation, growth, proliferation and/or propagation of cells under suitable conditions in a medium. Cells
15 are grown and maintained in a cell growth medium at an appropriate temperature and gas mixture. Culture conditions vary widely for each cell type. Typical growth conditions are a temperature of about 37°C, a CO₂ concentration of about 5% and a humidity of about 95%. Recipes for growth media can vary e.g. in pH, concentration of the carbon source (such as glucose), nature and concentration of growth factors, and the presence of other nutrients
20 (such as amino acids or vitamins). The growth factors used to supplement media are often derived from the serum of animal blood, such as fetal bovine serum (FBS), bovine calf serum (FCS), equine serum, and porcine serum. Cells can be grown either in suspension or as adherent cultures. There are also cell lines that have been modified to be able to survive in suspension cultures, so they can be grown to a higher density than adherent conditions
25 would allow.

[239] The term "expression" includes any step involved in the production of a construct of the invention including, but not limited to, transcription, post-transcriptional modification, translation, folding, post-translational modification, targeting to specific subcellular or extracellular locations, and secretion. The term "recovering" refers to a series of processes
30 intended to isolate the construct from the cell culture. The "recovering" or "purification" process may separate the protein and non-protein parts of the cell culture, and finally separate the desired construct from all other polypeptides and proteins. Separation steps usually exploit differences in protein size, physico-chemical properties, binding affinity and biological activity. Preparative purifications aim to produce a relatively large quantity of
35 purified proteins for subsequent use, while analytical purification produces a relatively small amount of a protein for a variety of research or analytical purposes.

[240] When using recombinant techniques, the construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. The construct of the invention may
5 e.g. be produced in bacteria such as *E. coli*. After expression, the construct is isolated from the bacterial cell paste in a soluble fraction and can be purified e.g. via affinity chromatography and/or size exclusion. Final purification can be carried out in a manner that is like the process for purifying a construct expressed in mammalian cells and secreted into the medium. Carter et al. (Biotechnology (NY) 1992 Feb;10(2):163-7) describe a procedure
10 for isolating antibodies which are secreted to the periplasmic space of *E. coli*.

[241] Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an ultrafiltration unit.

[242] The construct of the invention prepared from the host cells can be recovered or
15 purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography. Other techniques for protein purification such as fractionation on an ion-exchange column, mixed mode ion exchange, HIC, ethanol precipitation, size exclusion chromatography, reverse phase HPLC, chromatography on silica, chromatography on heparin sepharose, chromatography on an anion or cation exchange resin (such as a
20 polyaspartic acid column), immunoaffinity (such as Protein A/G/L) chromatography, chromato-focusing, SDS-PAGE, ultracentrifugation, and ammonium sulfate precipitation are also available depending on the construct to be recovered.

[243] A protease inhibitor may be included in any of the foregoing steps to inhibit proteolysis, and antibiotics may be included to prevent the growth of contaminants.

25 [244] Moreover, the invention provides a pharmaceutical composition or formulation comprising a polypeptide or polypeptide construct of the invention or a polypeptide or polypeptide construct produced according to the process of the invention.

[245] As used herein, the term "pharmaceutical composition" relates to a composition which is suitable for administration to a patient, preferably a human patient. The particularly
30 preferred pharmaceutical composition of this invention comprises one or a plurality of the construct(s) of the invention, preferably in a therapeutically effective amount. Preferably, the pharmaceutical composition further comprises suitable formulations of one or more (pharmaceutically effective) carriers, stabilizers, excipients, diluents, solubilizers, surfactants, emulsifiers, preservatives and/or adjuvants. Acceptable constituents of the composition are
35 preferably nontoxic to recipients at the dosages and concentrations employed.

Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

[246] The compositions may comprise a pharmaceutically acceptable carrier. In general, as used herein, "pharmaceutically acceptable carrier" means all aqueous and non-aqueous solutions, sterile solutions, solvents, buffers, e.g. phosphate buffered saline (PBS) solutions, water, suspensions, emulsions, such as oil/water emulsions, various types of wetting agents, liposomes, dispersion media and coatings, which are compatible with pharmaceutical administration, in particular with parenteral administration. The use of such media and agents in pharmaceutical compositions is well known in the art, and the compositions comprising such carriers can be formulated by well-known conventional methods.

[247] Certain embodiments provide pharmaceutical compositions comprising the construct of the invention and further one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used in the invention for a wide variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and/or to stabilize such formulations and processes against degradation and spoilage e.g. due to stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter. Excipients should in general be used in their lowest effective concentrations.

[248] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving certain characteristics of the composition such as the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration (see, Remington's Pharmaceutical Sciences, 18th Edition, 1990, Mack Publishing Company). In such embodiments, suitable formulation materials may include, but are not limited to:

- amino acids
- antimicrobials such as antibacterial and antifungal agents
- antioxidants
- buffers, buffer systems and buffering agents that are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a range of from about 5 to about 8 or 9
- non-aqueous solvents, vegetable oils, and injectable organic esters
- aqueous carriers including water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media
- biodegradable polymers such as polyesters
- bulking agents

- chelating agents
- isotonic and absorption delaying agents
- complexing agents
- fillers
- 5 • carbohydrates
- (low molecular weight) proteins, polypeptides or proteinaceous carriers, preferably of human origin
- coloring and flavouring agents
- sulfur containing reducing agents
- 10 • diluting agents
- emulsifying agents
- hydrophilic polymers
- salt-forming counter-ions
- preservatives
- 15 • metal complexes
- solvents and co-solvents
- sugars and sugar alcohols
- suspending agents
- surfactants or wetting agents
- 20 • stability enhancing agents
- tonicity enhancing agents
- parenteral delivery vehicles
- intravenous delivery vehicles

[249] It is common knowledge that the different constituents of the pharmaceutical composition can have different effects, for example, and amino acid can act as a buffer, a stabilizer and/or an antioxidant; mannitol can act as a bulking agent and/or a tonicity enhancing agent; sodium chloride can act as delivery vehicle and/or tonicity enhancing agent; etc.

[250] In the context of the present invention, a pharmaceutical composition may comprise:

- 30 (a) a polypeptide or polypeptide construct as described herein,
 (b) at least one buffer agent,
 (c) at least one saccharide, and
 (d) at least one surfactant;

wherein the pH of the pharmaceutical composition is in the range of 3.5 to 6.

[251] In the composition described above, the first domain preferably has an isoelectric point (pI) in the range of 4 to 9.5; the second domain has a pI in the range of 8 to 10, preferably 8.5 to 9.0; and the construct optionally comprises a third domain comprising two polypeptide monomers, each comprising a hinge, a CH2 domain and a CH3 domain, wherein
5 said two polypeptide monomers are fused to each other via a peptide linker.

[252] In the composition described above, it is further envisaged that the at least one buffer agent is present at a concentration range of 5 to 200 mM, more preferably at a concentration range of 10 to 50 mM. It is also envisaged that the at least one saccharide is selected from the group consisting of monosaccharide, disaccharide, cyclic polysaccharide, sugar alcohol,
10 linear branched dextran or linear non-branched dextran. It is also envisaged that the disaccharide is selected from the group consisting of sucrose, trehalose and mannitol, sorbitol, and combinations thereof. It is further envisaged that the sugar alcohol is sorbitol. It is also envisaged that the at least one saccharide is present at a concentration in the range of 1 to 15% (m/V), preferably in a concentration range of 9 to 12% (m/V). It is further
15 envisaged that the construct is present in a concentration range of 0.1 to 8 mg/ml, preferably of 0.2-2.5 mg/ml, more preferably of 0.25-1.0 mg/ml.

[253] According to one embodiment of the composition described above, the at least one surfactant is selected from the group consisting of polysorbate 20, polysorbate 40, polysorbate 60, polysorbate 80, poloxamer 188, pluronic F68, triton X-100, polyoxyethylen,
20 PEG 3350, PEG 4000 and combinations thereof. It is further envisaged that the at least one surfactant is present at a concentration in the range of 0.004 to 0.5 % (m/V), preferably in the range of 0.001 to 0.01% (m/V). It is envisaged that the pH of the composition is in the range of 4.0 to 5.0, preferably 4.2. It is also envisaged that the pharmaceutical composition has an osmolality in the range of 150 to 500 mOsm. It is further envisaged that the pharmaceutical
25 composition further comprises an excipient selected from the group consisting of one or more polyol(s) and one or more amino acid(s). It is envisaged in the context of the present invention that said one or more excipient is present in the concentration range of 0.1 to 15 % (w/V).

[254] The present invention also provides a pharmaceutical composition comprising (a) the
30 construct as described herein, preferably in a concentration range of 0.1 to 8 mg/ml, preferably of 0.2-2.5 mg/ml, more preferably of 0.25-1.0 mg/ml; (b) 10 mM glutamate or acetate; (c) 9% (m/V) sucrose or 6% (m/V) sucrose and 6% (m/V) hydroxypropyl- β -cyclodextrin; (d) 0.01% (m/V) polysorbate 80; wherein the pH of the liquid pharmaceutical composition is 4.2.

[255] It is envisaged that the composition of the invention might comprise, in addition to the
35 construct of the invention defined herein, further biologically active agents, depending on the

intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as cytostatica, drugs preventing hyperurikemia, drugs inhibiting immunoreactions, drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art. It is also envisaged that
5 the polypeptide construct of the present invention is applied in a co-therapy, i.e., in combination with another anti-cancer medicament.

[256] In this context, it is envisaged that the pharmaceutical composition of the invention (which comprises a construct comprising a CD3 binding domain and at least a further binding domain which binds to a cell surface target antigen, preferably a tumor antigen on the
10 surface of a target cell, as described in more detail herein above) furthermore comprises an agent, preferably an antibody or construct, which binds to a protein of the immune checkpoint pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). The present invention also refers to a combination of a polypeptide construct according to the invention (which comprises a construct comprising a CD3 binding domain
15 and at least a further binding domain which binds to a cell surface target antigen, preferably a tumor antigen on the surface of a target cell, as described in more detail herein above) and an agent, preferably an antibody or polypeptide construct, which binds to a protein of the immune checkpoint pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). Due to the nature of the at least two ingredients of the
20 combination, namely their pharmaceutical activity, the combination can also be referred to as a therapeutic combination. In some embodiments, the combination can be in the form of a pharmaceutical composition or of a kit. According to one embodiment, the pharmaceutical composition or the combination comprises a construct of the invention and an antibody or construct which binds to PD-1. Anti-PD-1 binding proteins useful for this purpose are e.g.
25 described in detail in PCT/US2019/013205 incorporated herein by reference.

[257] In certain embodiments, the optimal pharmaceutical composition is determined depending upon, for example, the intended route of administration, delivery format and desired dosage. See, for example, Remington's Pharmaceutical Sciences, supra. In certain
30 embodiments, such compositions may influence the physical state, stability, rate of in vivo release and rate of in vivo clearance of the construct of the invention. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection or physiological saline solution, possibly supplemented with other materials common in compositions for parenteral administration. In certain embodiments, the
35 compositions comprising the construct of the invention may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (Remington's Pharmaceutical Sciences, supra) in the form of a lyophilized cake or an

aqueous solution. Further, in certain embodiments, the construct of the invention may be formulated as a lyophilizate using appropriate excipients.

[258] When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired construct of the invention in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the construct of the invention is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent that may provide controlled or sustained release of the product which can be delivered via depot injection, or that may promote sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired construct.

[259] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving the construct of the invention in sustained or controlled delivery formulations. Techniques for formulating a variety of sustained- or controlled-delivery means are known to those skilled in the art. The construct may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, in colloidal drug delivery systems, or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

[260] Pharmaceutical compositions used for in vivo administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions are generally placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[261] Another aspect of the invention includes self-buffering formulations comprising the construct of the invention, which can be used as pharmaceutical compositions, as described in international patent application WO 2006/138181. A variety of publications are available on protein stabilization and formulation materials and methods useful in this regard, such as Arawaka T. et al., *Pharm Res.* 1991 Mar;8(3):285-91; Kendrick et al., "Physical stabilization of proteins in aqueous solution" in: *Rational Design of Stable Protein Formulations: Theory and Practice*, Carpenter and Manning, eds. *Pharmaceutical Biotechnology*. 13: 61-84 (2002), and Randolph and Jones, *Pharm Biotechnol.* 2002;13:159-75, see particularly the parts

pertinent to excipients and processes for self-buffering protein formulations, especially as to protein pharmaceutical products and processes for veterinary and/or human medical uses.

[262] Salts may be used in accordance with certain embodiments of the invention, e.g. to adjust the ionic strength and/or the isotonicity of a composition or formulation and/or to improve the solubility and/or physical stability of a construct or other ingredient of a composition in accordance with the invention. Ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive interactions. Ions also can stabilize the denatured state of a protein by binding to, particularly the denatured peptide linkages ($--CONH$) of the protein. Furthermore, ionic interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

[263] Ionic species differ significantly in their effects on proteins. Several categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as "kosmotropic". Destabilizing solutes are referred to as "chaotropic". Kosmotropes are commonly used at high concentrations to precipitate proteins from solution ("salting-out"). Chaotropes are commonly used to denature and/or to solubilize proteins ("salting-in"). The relative effectiveness of ions to "salt-in" and "salt-out" defines their position in the Hofmeister series.

[264] Free amino acids can be used in formulations or compositions comprising the construct of the invention in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as for other standard uses. Certain amino acids can be used for stabilizing proteins in a formulation, others are useful during lyophilization to ensure correct cake structure and properties of the active ingredient. Some amino acids may be useful to inhibit protein aggregation in both liquid and lyophilized formulations, and others are useful as antioxidants.

[265] Polyols are kosmotropic and are useful as stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols are also useful for adjusting the tonicity of formulations and for protecting against freeze-thaw stresses during transport or the preparation of bulks during the manufacturing process. Polyols can also serve as cryoprotectants in the context of the present invention.

- [266] Certain embodiments of the formulation or composition comprising the construct of the invention can comprise surfactants. Proteins may be susceptible to adsorption on surfaces and to denaturation and resulting aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These deleterious interactions generally scale inversely with protein concentration and are typically exacerbated by physical agitation, such as that generated during the shipping and handling of a product. Surfactants are routinely used to prevent, minimize, or reduce surface adsorption. Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein specific, since one specific surfactant will typically stabilize some proteins and destabilize others.
- [267] Certain embodiments of the formulation or composition comprising the construct of the invention can comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and temperature and by avoiding exposure to light. Antioxidant excipients can also be used to prevent oxidative degradation of proteins. It is envisaged that antioxidants for use in therapeutic protein formulations in accordance with the present invention can be water-soluble and maintain their activity throughout the shelf life of the product (the composition comprising the construct). Antioxidants can also damage proteins and should hence – among other things – be selected in a way to eliminate or sufficiently reduce the possibility of antioxidants damaging the construct or other proteins in the formulation.
- [268] Certain embodiments of the formulation or composition comprising the construct of the invention can comprise one or more preservatives. Preservatives are necessary for example when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that include preservatives can be challenging. Preservatives very often have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given preservative in the dosage form with

concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

- 5 [269] As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This shortens the time during which a preservative is in contact with the construct, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life. An important point to note is that preservative effectiveness should be demonstrated in the final
- 10 formulation containing the active drug and all excipient components. Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration.
- 15 [270] The biological activity of the pharmaceutical composition defined herein can be determined for instance by in vitro cytotoxicity assays, as described in the following examples, in WO 99/54440 or by Schlereth et al. (Cancer Immunol. Immunother. 20 (2005), 1-12). "Efficacy" or "in vivo efficacy" as used herein refers to the response to therapy by the pharmaceutical composition of formulation of the invention, using e.g. standardized NCI
- 20 response criteria. The success or in vivo efficacy of the therapy using a pharmaceutical composition of the invention refers to the effectiveness of the composition for its intended purpose, i.e. the ability of the composition to cause its desired effect, i.e. depletion of pathologic cells, e.g. tumor cells. The in vivo efficacy may be monitored by established standard methods for the respective disease entities including, but not limited to, white blood
- 25 cell counts, differentials, fluorescence activated cell sorting, bone marrow aspiration. In addition, various disease specific clinical chemistry parameters and other established standard methods may be used. Furthermore, computer-aided tomography, X-ray, nuclear magnetic resonance tomography, positron-emission tomography scanning, lymph node biopsies/histologies and other established standard methods may be used.
- 30 [271] Another major challenge in the development of drugs such as the pharmaceutical composition of the invention is the predictable modulation of pharmacokinetic properties. To this end, a pharmacokinetic profile of the drug candidate, i.e. a profile of the pharmacokinetic parameters that affect the ability of a specific drug to treat a given condition, can be established. Pharmacokinetic parameters of the drug influencing the ability of a drug for
- 35 treating a certain disease entity include, but are not limited to: half-life, volume of distribution,

hepatic first-pass metabolism and the degree of blood serum binding. The efficacy of a given drug agent can be influenced by each of the parameters mentioned above.

[272] "Half-life" is the time required for a quantity to reduce to half its initial value. The medical sciences refer to the half-life of substances or drugs in the human body. In a medical context, half-life may refer to the time it takes for a substance / drug to lose one-half of its activity, e.g. pharmacologic, physiologic, or radiological activity. The half-life may also describe the time that it takes for the concentration of a drug or substance (e.g., a construct of the invention) in blood plasma / serum to reach one-half of its steady-state value ("serum half-life"). Typically, the elimination or removal of an administered substance / drug refers to the body's cleansing through biological processes such as metabolism, excretion, also involving the function of kidneys and liver. The "first-pass metabolism" is a phenomenon of drug metabolism whereby the concentration of a drug is reduced before it reaches the circulation. It is the fraction of drug lost during the process of absorption. Accordingly, by "hepatic first-pass metabolism" is meant the propensity of a drug to be metabolized upon first contact with the liver, i.e. during its first pass through the liver. "Volume of distribution" (VD) means the degree to which a drug is distributed in body tissue rather than the blood plasma, a higher VD indicating a greater amount of tissue distribution. The retention of a drug can occur throughout the various compartments of the body, such as intracellular and extracellular spaces, tissues and organs, etc. "Degree of blood serum binding" means the propensity of a drug to interact with and bind to blood serum proteins, such as albumin, leading to a reduction or loss of biological activity of the drug.

[273] Pharmacokinetic parameters also include bioavailability, lag time (T lag), Tmax, absorption rates, and/or Cmax for a given amount of drug administered. "Bioavailability" refers to the fraction of an administered dose of a drug / substance that reaches the systemic circulation (the blood compartment). When a medication is administered intravenously, its bioavailability is considered to be 100%. However, when a medication is administered via other routes (such as orally), its bioavailability generally decreases. "Lag time" means the time delay between the administration of the drug and its detection and measurability in blood or plasma. Cmax is the maximum plasma concentration that a drug achieves after its administration (and before the administration of a second dose). Tmax is the time at which Cmax is reached. The time to reach a blood or tissue concentration of the drug which is required for its biological effect is influenced by all parameters. Pharmacokinetic parameters of constructs exhibiting cross-species specificity may be determined in preclinical animal testing in non-chimpanzee primates as outlined above and set forth e.g. in Schlereth et al. (supra).

[274] One embodiment provides the construct of the invention (or the construct produced according to the process of the invention), for the use as a medicament, particularly for the use in the prevention, treatment or amelioration (preferably treatment) of a disease, preferably a tumorous disease, more preferred a neoplasm, cancer or tumor. Another
5 embodiment provides the use of the construct of the invention (or of the construct produced according to the process of the invention) in the manufacture of a medicament for the prevention, treatment or amelioration of a disease, preferably a tumorous disease, more preferred a neoplasm, cancer or tumor. It is also envisaged to provide a method for the prevention, treatment or amelioration of a disease, preferably a tumorous disease, more
10 preferred a neoplasm, cancer or tumor, comprising the step of administering to a subject in need thereof the construct of the present invention (or the construct produced according to the process of the present invention). The terms "subject in need", "patient" or those "in need of treatment" include those already with the disease, as well as those in which the disease is to be prevented. The terms also include human and other mammalian subjects that receive
15 either prophylactic or therapeutic treatment.

[275] The polypeptides/polypeptide constructs of the invention and the formulations / pharmaceutical compositions described herein are useful in the treatment, amelioration and/or prevention of the medical condition as described herein in a patient in need thereof. The term "treatment" refers to both therapeutic treatment and prophylactic or preventative
20 measures. Treatment includes the application or administration of the polypeptides/polypeptide constructs / pharmaceutical composition to the body, to an isolated tissue, or to a cell from a patient or a subject in need who has a disease/disorder as described herein, a symptom of such disease/disorder, or a predisposition toward such disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate,
25 improve, or affect the disease, the symptom of the disease, or the predisposition toward the disease. The term "amelioration" as used herein refers to any improvement of the disease state of a patient, by the administration of a polypeptide construct according to the invention to such patient or subject in need thereof. Such an improvement may be a slowing down or stopping of the progression of the disease of the patient, and/or as a decrease in severity of
30 disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease. The term "prevention" as used herein means the avoidance of the occurrence or of the re-occurrence of a disease as specified herein, by the administration of a construct according to the invention to a subject in need thereof.

35 [276] The term "disease" refers to any condition that would benefit from treatment with the construct or the pharmaceutical composition described herein. This includes chronic and acute disorders or diseases including those pathological conditions that predispose the

mammal to the disease in question. The disease is preferably a tumorous disease, more preferred a neoplasm, cancer or tumor. The disease, neoplasm, cancer or tumor is preferably positive for a tumor antigen, preferably such as those defined herein above, i.e. it is characterized by expression or overexpression of a tumor antigen, preferably such as those defined herein above. An overexpression of a tumor antigen means that there is an increase by at least 10%, in particular at least 25%, at least 50%, at least 100%, at least 250%, at least 500%, at least 750%, at least 1000% or even more. Expression is, preferably, only found in a diseased tissue, while expression in a corresponding healthy tissue is not or significantly not detectable. According to the invention, diseases associated with cells expressing a tumor antigen, preferably such as those defined herein above, include cancer diseases. Furthermore, according to the invention, cancer diseases preferably are those wherein the cancer cells express a tumor antigen. In accordance with the invention, the disease, preferably tumorous disease, more preferred neoplasm, tumor or cancer is preferably characterized by the presence of BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive cells. In other words, the tumorous disease, more preferred neoplasm, tumor or cancer is preferably associated with the presence of BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive cells; the tumorous disease, more preferred neoplasm, tumor or cancer can therefore be termed a BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive neoplasm, tumor or cancer. It is understood herein, that each of said tumor antigen-positive neoplasms, tumors or cancers can be prevented, treated or ameliorated using a polypeptide or polypeptide construct according to the invention that comprises a binding domain against the tumor antigen expressed by the cells with which said neoplasm, tumor or cancer is associated with. A BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive neoplasm, tumor or cancer

can be prevented, treated or ameliorated using a polypeptide or polypeptide construct according to the invention that comprises a binding domain against BCMA (for a BCMA-positive neoplasm, tumor or cancer), CD123 (for a CD123-positive neoplasm, tumor or cancer), CD19 (for a CD19-positive neoplasm, tumor or cancer), CD20 (for a CD20-positive neoplasm, tumor or cancer), CD22 (for a CD22-positive neoplasm, tumor or cancer), CD33 (for a CD33-positive neoplasm, tumor or cancer), CD70 (for a CD70-positive neoplasm, tumor or cancer), CDH19 (for a CDH19-positive neoplasm, tumor or cancer), CDH3 (for a CDH3-positive neoplasm, tumor or cancer), CLL1 (for a CLL1-positive neoplasm, tumor or cancer), CS1 (for a CS1-positive neoplasm, tumor or cancer), CLDN6 (for a CLDN6-positive neoplasm, tumor or cancer), CLDN18.2 (for a CLDN18.2-positive neoplasm, tumor or cancer), DLL3 (for a DLL3-positive neoplasm, tumor or cancer), EGFRvIII (for a EGFRvIII-positive neoplasm, tumor or cancer), FLT3 (for a FLT3-positive neoplasm, tumor or cancer), MAGEB2 (for a MAGEB2-positive neoplasm, tumor or cancer), MART1 (for a MART1-positive neoplasm, tumor or cancer), MSLN (for a MSLN-positive neoplasm, tumor or cancer), MUC17 (for a MUC17-positive neoplasm, tumor or cancer), PSMA (for a PSMA-positive neoplasm, tumor or cancer), and STEAP1 (for a STEAP1-positive neoplasm, tumor or cancer), respectively.

[277] A “neoplasm” is an abnormal growth of tissue, usually but not always forming a mass. When also forming a mass, it is commonly referred to as a “tumor”. Neoplasms or tumors can be benign, potentially malignant (pre-cancerous), or malignant (cancerous). Malignant neoplasms / tumors are commonly called cancer. They usually invade and destroy the surrounding tissue and may form metastases, i.e., they spread to other parts, tissues or organs of the body. A “primary tumor” is a tumor growing at the anatomical site where tumor progression began and proceeded to yield a cancerous mass. Most cancers develop at their primary site but then go on to metastasize or spread to other parts (e.g. tissues and organs) of the body. These further tumors are “secondary tumors”. Most cancers continue to be called after their primary site, even after they have spread to other parts of the body.

[278] Lymphomas and leukemias are lymphoid neoplasms. For the purposes of the present invention, they are also encompassed by the terms “tumor” and “cancer”. For the purposes of the present invention, the terms “neoplasm”, “tumor” and “cancer” may be used interchangeably, and they comprise both primary tumors / cancers and secondary tumors / cancers (or “metastases”) as well as mass-forming neoplasms (tumors) and lymphoid neoplasms (such as lymphomas and leukemias), and minimal residual disease (MRD).

[279] The term “minimal residual disease” (MRD) refers to the evidence for the presence of small numbers of residual cancer cells that remain in the patient after cancer treatment, e.g. when the patient is in remission (no symptoms or signs of disease). A very small number of

remaining cancer cells usually cannot be detected by routine means because the standard tests used to assess or detect cancer are not sensitive enough to detect MRD. Nowadays, very sensitive molecular biology tests for MRD are available, such as flow cytometry, PCR and next-generation sequencing. These tests can measure minimal levels of cancer cells in
5 tissue samples, sometimes as low as one cancer cell in a million normal cells. In the context of the present invention, the terms "prevention", "treatment" or "amelioration" of a cancer are envisaged to also encompass "prevention, treatment or amelioration of MRD", whether the MRD was detected or not.

[280] The construct of the invention will generally be designed for specific routes and
10 methods of administration, for specific dosages and frequencies of administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. The materials of the composition are preferably formulated in concentrations that are acceptable for the site of administration. Formulations and compositions thus may be designed in accordance with the invention for delivery by any suitable route of administration.
15 In the context of the present invention, the routes of administration include, but are not limited to topical routes, enteral routes and parenteral routes.

[281] If the pharmaceutical composition has been lyophilized, the lyophilized material is first reconstituted in an appropriate liquid prior to administration. The lyophilized material may be reconstituted in, e.g., bacteriostatic water for injection (BWFI), physiological saline,
20 phosphate buffered saline (PBS), or the same formulation the protein had been in prior to lyophilization. The pharmaceutical compositions and the construct of this invention are particularly useful for parenteral administration, e.g., intravenous delivery, for example by injection or infusion. Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are
25 described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447,233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163.

[282] The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. in dose escalating studies. As set forth above,
30 the construct of the invention exhibiting cross-species specificity as described herein can also be advantageously used in in preclinical testing in non-chimpanzee primates. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical art, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the specific compound to be administered, sex,
35 time and route of administration, general health, and other drugs being administered concurrently.

[283] An “effective dose” is an amount of a therapeutic agent that is sufficient to achieve or at least partially achieve a desired effect. A “therapeutically effective dose” is an amount that is sufficient to cure or at least partially arrest the disease and its complications, signs and symptoms in a patient suffering from the disease. Amounts or doses effective for this use will
5 depend on the disease to be treated (the indication), the delivered construct, the therapeutic context and objectives, the severity of the disease, prior therapy, the patient's clinical history and response to the therapeutic agent, the route of administration, the size (body weight, body surface) and/or condition (the age and general health) of the patient, and the general state of the patient's own immune system. The proper dose can be adjusted according to the
10 judgment of the attending physician, to obtain the optimal therapeutic effect.

[284] A therapeutically effective amount of a construct of the invention preferably results in a decrease in severity of disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease. In the treatment of tumor antigen-expressing tumors, a therapeutically effective amount of the
15 construct of the invention comprising a binding domain against said tumor antigen preferably inhibits tumor cell growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may also be evaluated in an animal model predictive of efficacy in human tumors.

[285] In a further embodiment, the invention provides a kit comprising a construct of the invention, a construct produced according to the process of the invention, a polynucleotide of the invention, a vector of the invention, and/or a host cell of the invention. In the context of the present invention, the term “kit” means two or more components – one of which
25 corresponding to the construct, the pharmaceutical composition, the polynucleotide, the vector or the host cell of the invention – packaged together in a container, recipient or otherwise. A kit can hence be described as a set of products and/or utensils that are sufficient to achieve a certain goal, which can be marketed as a single unit.

[286] It is envisaged that a further component of the kit of the invention is an agent, preferably an antibody or construct, which binds to a protein of the immune checkpoint
30 pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). These agents are described in more detail herein above. According to one embodiment, the kit comprises a construct of the invention and an antibody or construct which binds to PD-1. Anti-PD-1 binding proteins useful for this purpose are e.g. described in detail in PCT/US2019/013205. In certain embodiment, the kit allows for the simultaneous
35 and/or sequential administration of the components.

[287] The kit may comprise one or more recipients (such as vials, ampoules, containers, syringes, bottles, bags) of any appropriate shape, size and material (preferably waterproof, e.g. plastic or glass) containing the construct or the pharmaceutical composition of the present invention in an appropriate dosage for administration (see above). The kit may additionally contain directions for use (e.g. in the form of a leaflet or instruction manual), means for administering the construct or the pharmaceutical composition of the present invention such as a syringe, pump, infuser or the like, means for reconstituting the construct of the invention and/or means for diluting the construct of the invention.

[288] The invention also provides kits for a single-dose administration unit. The kit of the invention may also contain a first recipient comprising a dried / lyophilized construct or pharmaceutical composition and a second recipient comprising an aqueous formulation. In certain embodiments of this invention, kits containing single-chambered and multi-chambered pre-filled syringes are provided.

[289] Whenever the term “construct” is used herein, said term refers to the used polypeptide/polypeptide constructs of the invention or controls thereof as indicated.

[290] As used herein, the singular forms “a”, “an”, and “the” include plural references unless the context clearly indicates otherwise. Thus, for example, reference to “a reagent” includes one or more of such different reagents and reference to “the method” includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

[291] Unless otherwise indicated, the term “at least” preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

[292] The term “and/or” wherever used herein includes the meaning of “and”, “or” and “all or any other combination of the elements connected by said term”.

[293] The term “about” or “approximately” as used herein means within $\pm 20\%$, preferably within $\pm 15\%$, more preferably within $\pm 10\%$, and most preferably within $\pm 5\%$ of a given value or range. It also includes the concrete value, e.g., “about 50” includes the value “50”.

[294] Throughout this specification and the claims, unless the context requires otherwise, the word “comprise”, and variations such as “comprises” and “comprising”, will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term

“comprising” can be substituted with the term “containing” or “including” or sometimes when used herein with the term “having”.

5 [295] When used herein “consisting of” excludes any element, step, or ingredient not specified in the claim element. When used herein, “consisting essentially of” does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

[296] In each instance herein, any of the terms “comprising”, “consisting essentially of” and “consisting of” may be replaced with either of the other two terms.

10 [297] The above description and the below examples provide exemplary arrangements, but the present invention is not limited to the specific methodologies, techniques, protocols, material, reagents, substances, etc., described herein and as such can vary. The terminology used herein serves to describe specific embodiments only. The terminology used herein does not intend to limit the scope of the present invention, which is defined solely by the claims. Aspects of the invention are provided in the independent claims. Some optional
15 features of the invention are provided in the dependent claims.

[298] All publications and patents cited throughout the text of this specification (including all patents, patent applications, scientific publications, manufacturer’s specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to
20 antedate such disclosure by virtue of prior invention. To the extent the material incorporated by reference contradicts or is inconsistent with this specification, the specification will supersede any such material.

[299] A better understanding of the present invention and of its advantages will be obtained from the following examples, offered for illustrative purposes only. The examples are not
25 intended and should not be construed as to limit the scope of the present invention in any way.

Brief Description of the Drawings:

[300] Figure 1 A): Effector cells: human unstimulated T cells; Target cells: CHO hu CD70 pEFDHR

Legend:

- 5 I2C: CD70 1-A9D CC x I2C x scFc
- I2CA: CD70 1-A9D CC x I2C H109A x scFc
- 8A8.04: CD70 1-A9D CC x 8A8.04 x scFc
- 5C3.04: CD70 1-A9D CC x 5C3.04 x scFc
- I2E: CD70 1-A9D CC x 5C3.01 x scFc
- 10 I2K: CD70 1-A9D CC x 5G6.05 x scFc
- 5G6.04: CD70 1-A9D CC x 5G6.04 x scFc
- 5G6.03: CD70 1-A9D CC x 5G6.03 x scFc
- 1D5.04: CD70 1-A9D CC x 1D5.04 x scFc
- 8A8.02: CD70 1-A9D CC x 8A8.02 x scFc
- 15 1D5.03: CD70 1-A9D CC x 1D5.03 x scFc

[301] Figure 1 B): Effector cells: human unstimulated T cells; Target cells: hu ori FLT3 v1 co CHO #12

Legend:

- I2C: FL 7-H3 CC x I2C x scFc
- 20 5G6.04: FL 7-H3 CC x 5G6.04 x scFc
- 8A8.04: FL 7-H3 CC x 8A8.04 x scFc
- 5C3.04: FL 7-H3 CC x 5C3.04 x scFc
- I2E: FL 7-H3 CC x 5C3.01 x scFc
- I2K: FL 7-H3 CC x 5G6.05 x scFc
- 25 I2C CC 44/100: FL 7-H3 CC x I2C CC 44/100 x scFc

Examples

[302] Example 1: Thermal stability

[303] Purified monomeric BiTE® protein at 1 mg/ml formulated in screening buffer was analysed. Thermal stability was determined by Dynamic Light Scattering DLS and Differential Scanning Fluorometry DSF.

[304] DLS

100 µl protein solution were transferred in doubles in a multi well plate, overlaid with paraffin oil and placed in a DLS plate reader (DynaPro Plate Reader II with temperature control, Wyatt Technology Europe GmbH, Dernbach – Germany). Thermal stability was determined in a linear increasing temperature scan from 40°C to 70°C while measuring the hydrodynamic radius at the different temperatures in this range. Aggregation temperature was defined at the temperature the radius begins to expand. The mean of both determined aggregation temperatures was calculated and used for candidate ranking.

[305] DSF

Three glass capillaries were filled each with approx. 40 µl protein solution and placed simultaneously into a DSF reader with temperature control (Prometheus nanoDSF, NanoTemper Technologies GmbH, Munich - Germany). Protein internal fluorescence was measured at an excitation wavelength of 280 nm and emission wavelengths 330 and 350 nm in a linear increasing temperature scan from 20°C to 95°C. Changes in the ratio of the two emission wavelength intensities indicate conformational changes in the protein therefore showing the melting temperature(s) of the analyzed BiTE proteins. The first maximum of the first derivate of the ratio 350/330 nm curve was defined as first melting temperature. The mean of all three determined first melting temperatures was calculated and used for candidate ranking.

[306] The incorporation of specific amino acid mutations in the sequence of the anti-CD3 binder I2C (VH and VL defined in SEQ ID NO: 1854 and 1855, respectively, and linked with a peptide linker of SEQ ID NO: 2; CD70 target binder VH and VL defined in SEQ ID NOs: 2185 and 2186, respectively, and linked with a peptide linker of SEQ ID NO: 2; CD70 binding domain linked to CD3 binding domain with linker of SEQ ID NO: 6; HLE domain as specified in SEQ ID NO: 18 linked with a G4 linker to the C-terminus of the VL region of the CD3 binder; CD70 binding domain is at the N-terminus, followed by the CD3 binding domain with the HLE domain at the C-terminus of the BiTE® molecule) in the BiTE-HLE context resulted in aggregation temperature values of 57.5°C to 62.0 °C determined by Dynamic Light Scattering (DLS) and melting temperature values of 62.9 °C to 70.3 °C determined by Differential scanning Fluorometry (DSF). The BiTE-HLE molecules harboring the I2C variants

showed an aggregation temperature increase of 2.3 °C to 6.8 °C in comparison to the unmodified I2C. The same effect was observed in the melting temperature measurements of the I2C variants resulting in an increase of 2.1 °C to 9.5 °C as compared to the unmodified I2C.

- 5 **[307]** Also the BiTE-HLE construct containing the anti-CD3 binder variant I2C CC44/100, in which an additional disulfide bond was engineered for stabilizing (Reiter, Y. et al., 1994) by replacing the amino acid residues with Cysteine residues at position 44 in the heavy chain variable region and at position 100 in the light chain variable region (numbering scheme according to Kabat et al., 1991), showed a thermostability increase of 3.2 °C for DLS and 5.3
- 10 °C for DSF as compared to the unmodified I2C. However, said BiTE®-HLE construct exhibited a significantly decreased cytotoxic activity (see further example) resulting in a construct which is therefore not suitable for further development and use as a part of T cell engagers.

[308]

CD3 binder	Thermostability		
in CD70 BiTE-HLE	DLS aggregation [°C]	DSF melting [°C]	CD3 binding domain SEQ ID NOs: VH, VL, linker
I2E	59,4	68,7	2012, 2013, 2
I2K	58,8	64,6	2020, 2021, 2
I2L	60,4	69,3	2028, 2029, 2
I2M	60,3	67,3	2036, 2037, 2
I2M2	58,9	66,9	2044, 2045, 2
1D5.01	62,0	70,3	42, 43, 2
1D5.03	61,5	70,0	50, 51, 2
1D5.04	61,8	69,7	58, 59, 2
4G10.04	59,4	66,0	66, 67, 2
5B1.05	58,6	67,8	74, 75, 2
5B1.09	58,8	68,2	82, 83, 2
5C3.04	60,6	69,2	90, 91, 2
5C3.05	60,5	69,2	98, 99, 2
5G6.03	60,1	67,4	100, 101, 2
5G6.04	59,3	65,5	108, 109, 2
6H10.03	60,0	67,3	116, 117, 2
8A8.02	59,4	65,9	26, 27, 2
8A8.04	59,3	67,0	34, 35, 2
I2C CC44/100	58,4	66,1	
I2C H109A	57,5	62,9	2560, 2561, 2
I2C	55,2	60,8	1854, 1855, 2

Table 2: Aggregation and melting temperatures of BiTE-HLE molecules harboring various CD3 binding domains determined by Dynamic Light Scattering (DLS) or Differential scanning Fluorometry (DSF), respectively.

[309] The mutation of single or more amino acids in the sequence of the anti-CD3 binder I2C in the BiTE-HLE context resulted in aggregation temperature values of 57.0°C to 62.4°C determined by Dynamic Light Scattering (DLS) and melting temperature values of 62.1°C to 68.8°C determined by Differential scanning Fluorometry (DSF). The BiTE-HLE molecules harboring the I2C mutants showed an aggregation temperature increase of 1.8°C to 7.2°C in comparison to the unmodified I2C. The same effect was observed in the melting temperature measurements of the I2C mutants resulting in an increase of 1.0°C to 7.7°C as compared to the unmodified I2C. The CD3 binder as referenced in the below Table specifies the amino acid residue exchanges and their positions in the first column; for each entry it is shown in brackets the positions as used in reference to the base sequence of the VH region sequence as defined in SEQ ID NO: 1854 and the VL region sequence as defined in SEQ ID NO: 1855 which is the authoritative nomenclature in accordance with the invention.

CD3 binder	Thermostability		CD3 binding domain SEQ ID NOs: VH, VL, linker
in CD70 BiTE-HLE	DLS aggregation [°C]	DSF melting [°C]	
I2C_HC_A89V_V107A_LC_L21I_Q46K_L83S_G141S (I2C_HC_A81V_V99A_LC_L20I_Q40K_L69S_G102S)	61,0	68,8	
I2C_HC_M41I_A89V_LC_L21I_Q46K_G141S (I2C_HC_M34I_A81V_LC_L20I_Q40K_G102S)	62,4	68,6	1898, 1899, 2
I2C_HC_M41I_LC_L21I_Q46K_G141S (I2C_HC_M34I_LC_L20I_Q40K_G102S)	61,9	68,3	1904, 1905, 2
I2C_HC_M41I_Q46E_A89V_LC_L21I_Q46K_G141S (I2C_HC_M34I_Q39E_A81V_LC_L20I_Q40K_G102S)	61,4	68,2	1906, 1907, 2
I2C_HC_M41I_A89V_LC_Q46K (I2C_HC_M34I_A81V_LC_Q40K)	60,5	66,6	1900, 1901, 2
I2C_HC_L52M_LC_L21I_Q46K_G141S (I2C_HC_L45M_LC_L20I_Q40K_G102S)	58,6	65,7	1866, 1867, 2
I2C_HC_M41I_S73A_H109A_N114S (I2C_HC_M34I_S65A_H101A_N106S)	59,0	65,4	
I2C_LC_L21I_Q46K_L83S_G141S (I2C_LC_L20I_Q40K_L69S_G102S)	59,0	65,3	
I2C_HC_M41F_A89V (I2C_HC_M34F_A81V)	59,3	65,0	1884, 1885, 2
I2C_HC_L52M_LC_Q46K_G141S (I2C_HC_L45M_LC_Q40K_G102S)	59,5	65,0	1870, 1871, 2
I2C_HC_Q46D_LC_L21I_Q46K_G141S (I2C_HC_Q39D_LC_L20I_Q40K_G102S)	58,3	64,7	1918, 1919,2
I2C_HC_M41I_A89V (I2C_HC_M34I_A81V)	59,1	64,3	1896, 1897,

			2
I2C_HC_Q46E_LC_L21I_Q46K_G141S (I2C_HC_Q39E_LC_L20I_Q40K_G102S)	58,9	64,3	1932, 1933, 2
I2C_HC_L52M_LC_Q46K (I2C_HC_L45M_LC_Q40K)	58,9	64,3	1868, 1869, 2
I2C_HC_M41I_S73A_A89V_V107A_H109A_N114S (I2C_HC_M34I_S65A_A81V_V99A_H101A_N106S)	58,1	64,2	
I2C_HC_Q46D_LC_L21I_Q46R_G141S (I2C_HC_Q39D_LC_L20I_Q40R_G102S)	58,2	63,7	1928, 1929, 2
I2C_HC_M41I (I2C_HC_M34I)	58,2	63,6	1892, 1893, 2
I2C_LC_Q46K (I2C_LC_Q40K)	58,4	63,5	1974, 1975, 2
I2C_HC_Q46D_LC_Q46K_G141S (I2C_HC_Q39D_LC_Q40K_G102S)	58,2	63,5	1922, 1923, 2
I2C_LC_L21I_G141S (I2C_LC_L20I_G102S)	57,4	63,2	
I2C_HC_Q46K (I2C_HC_Q39K)	57,4	63,2	1944, 1945, 2
I2C_HC_Q46E_LC_Q46K_G141S (I2C_HC_Q39E_LC_Q40K_G102S)	58,0	63,2	1938, 1939, 2
I2C_HC_Q46E_LC_L21I_Q46R_G141S (I2C_HC_Q39E_LC_L20I_Q40R_G102S)	57,9	63,0	1934, 1935, 2
I2C_HC_Q46D_LC_Q46R_G141S (I2C_HC_Q39D_LC_Q40R_G102S)	57,3	62,9	1926, 1927, 2
I2C_HC_A89V (I2C_HC_A81V)	58,2	62,9	1862, 1863, 2
I2C_HC_Q46D_LC_Q46K (I2C_HC_Q39D_LC_Q40K)	57,1	62,8	1920, 1921, 2
I2C_HC_W136F (I2C_HC_W112F)	57,0	62,7	1958, 1959, 2
I2C_HC_W136F_LC_V44I (I2C_HC_W112F _LC_V38I)	57,8	62,4	1960, 1961, 2
I2C_HC_Q46E_LC_Q46K (I2C_HC_Q39E_LC_Q40K)	58,2	62,3	1936, 1937, 2
I2C_HC_M41V (I2C_HC_M34V)	57,6	62,1	1914, 1915, 2
I2C	55,2	60,8	

Table 3: Aggregation and melting temperatures of BiTE-HLE molecules harboring the CD3 binding domain "I2C" (SEQ ID NO: 1854 and 1855, respectively, linked by peptide linker (G₄S)₃ (SEQ ID NO: 2)), respectively) with several amino acid mutations determined by Dynamic Light Scattering (DLS) or Differential scanning Fluorometry (DSF), respectively, as described herein above.

5

[310]

[311] Example 2: Cytotoxic activity

[312] Cytotoxic activity

Human peripheral blood mononuclear cells (PBMC) were prepared by Ficoll density gradient centrifugation from enriched lymphocyte preparations (buffy coats), a side product of blood banks collecting blood for transfusions. Buffy coats were supplied by a local blood bank and PBMC were prepared on the same day of blood collection. After Ficoll density centrifugation and extensive washes with Dulbecco's PBS (Gibco), remaining erythrocytes were removed from PBMC via incubation with erythrocyte lysis buffer (155 mM NH_4Cl , 10 mM KHCO_3 , 100 μM EDTA). Platelets were removed via the supernatant upon centrifugation of PBMC at 100 x g. Remaining lymphocytes mainly encompass B and T lymphocytes, NK cells and monocytes. PBMC were kept in culture at 37°C/5% CO_2 in RPMI medium (Gibco) with 10% FCS (Gibco).

[313] Depletion of CD14⁺ and CD56⁺ cells

For depletion of CD14⁺ cells, human CD14 MicroBeads (Milty Biotec, MACS, #130-050-201) were used, for depletion of NK cells human CD56 MicroBeads (MACS, #130-050-401). PBMC were counted and centrifuged for 10 min at room temperature with 300 x g. The supernatant was discarded and the cell pellet resuspended in MACS isolation buffer [80 μL /10⁷ cells; PBS (Invitrogen, #20012-043), 0.5% (v/v) FBS (Gibco, #10270-106), 2 mM EDTA (Sigma-Aldrich, #E-6511)]. CD14 MicroBeads and CD56 MicroBeads (20 μL /10⁷ cells) were added and incubated for 15 min at 4 - 8°C. The cells were washed with MACS isolation buffer (1 - 2 mL/10⁷ cells). After centrifugation (see above), supernatant was discarded and cells resuspended in MACS isolation buffer (500 μL /10⁸ cells). CD14/CD56 negative cells were then isolated using LS Columns (Milty Biotec, #130-042-401). PBMC w/o CD14⁺/CD56⁺ cells were cultured in RPMI complete medium i.e. RPMI1640 (Biochrom AG, #FG1215) supplemented with 10% FBS (Biochrom AG, #S0115), 1x non-essential amino acids (Biochrom AG, #K0293), 10 mM Hepes buffer (Biochrom AG, #L1613), 1 mM sodium pyruvate (Biochrom AG, #L0473) and 100 U/mL penicillin/streptomycin (Biochrom AG, #A2213) at 37°C in an incubator until needed.

[314] **Target cell labeling**

For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye DiOC₁₈ (DiO) (Molecular Probes, #V22886) was used to label human target-transfected CHO cells as target cells and distinguish them from effector cells. Briefly, cells were harvested, washed once with PBS and adjusted to 10⁶ cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 μL /10⁶ cells). After incubation for 3 min at 37°C, cells were washed twice in complete RPMI medium and the cell number adjusted to 1.25 x 10⁵ cells/mL. The vitality of cells was determined using the NC-250 cell counter (Chemometec).

[315] Flow cytometry based analysis

This assay was designed to quantify the lysis of human target-transfected CHO cells in the presence of serial dilutions of anti-target multi-specific constructs. Equal volumes of DiO-labeled target cells and effector cells (i.e., PBMC w/o CD14⁺ and CD56⁺ cells) were mixed, resulting in an E:T cell ratio of 10:1. 80 µl of this suspension were transferred to each well of a 96-well plate. 20 µL of serial dilutions of the anti-target x anti-CD3 multi-specific constructs and a negative control (a CD3-based multi-specific construct recognizing an irrelevant target antigen) or RPMI complete medium as an additional negative control were added. The multi-specific construct-mediated cytotoxic reaction proceeded for 48 hours in a 7% CO₂ humidified incubator. Then cells were transferred to a new 96-well plate and loss of target cell membrane integrity was monitored by adding propidium iodide (PI) at a final concentration of 1 µg/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

[316] Samples were measured by flow cytometry on an iQue Plus instrument and analyzed by Forecyt software (both from Intellicyt). Target cells were identified as DiO-positive cells. PI-negative target cells were classified as living target cells. Percentage of cytotoxicity was calculated according to the following formula:

$$\text{Cytotoxicity [\%]} = \frac{n_{\text{dead target cells}}}{n_{\text{target cells}}} \times 100$$

n = number of events

Using GraphPad Prism 6 software (Graph Pad Software, San Diego), the percentage of cytotoxicity was plotted against the corresponding bispecific construct concentrations. Dose response curves were analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC50 values were calculated.

[317] Results:

[318] Table 4: EC50 values in pM of T-cell engager with different anti-CD3 scFvs

	EC50 [pM]
I2C	0.2
I2CA	1.2
8A8.04	0.1

5C3.04	0.1
I2E	0.05
I2K	0.1
5G6.04	0.1
5G6.03	0.1
1D5.04	0.4
8A8.02	0.1
1D5.03	0.2

[319] T-cell engager with anti-CD3 scFvs I2C, I2CA, 8A8.04, 5C3.04, I2E, I2K, 5G6.04, 5G6.03, 1D5.04, 8A8.02 and 1D5.03 show similar EC50 values in range from 0.05 pM to 0.4 pM (Fig. 1 A) and Table 4).

5

[320] Table 5: EC50 values in pM of T-cell engager with different anti-CD3 scFvs

[321]

	EC50 [pM]
I2C	5.3
5G6.04	5.1
8A8.04	7.0
I2E	4.5
I2K	4.5
I2C CC 44/100	1578

[322] T-cell engager with anti-CD3 scFvs I2C, 5G6.04, 8A8.04, I2E and I2K show similar EC50 values in the range from 4.5 pM to 7.0 pM. T-cell engager with anti-CD3 scFv I2C CC 44/100 shows an EC50 value of 1578 pM and is 297-fold less active compared to T-cell engager with anti-CD3 scFv I2C (Fig. 1 B) and Table 5).

10

Sequences

[324] The below sequence list is the authoritative list for SEQ ID NOs referred to in the specification text and claims and may contain (a) gap(s) as to consecutive numbering. Any further list, such as the list complying with WIPO Standard ST.25 that contains consecutive

5 numberings has been generated of this list and the difference in Sequence numbers is to be reconciled with the below list. Sequence identity can be identified without further ado by reference to the unique entry in the second column identified as “designation” as well as a sequence alignment.:

[illegible]

118

46	16281-D5.3 - HCDR3	artificial	AGNFGSSYISYFAY
47	16281-D5.3 - LCDR1	artificial	GSSTGAVTSGNYPN
48	16281-D5.3 - LCDR2	artificial	GTKFLAP
49	16281-D5.3 - LCDR3	artificial	ALWYSNRWV
50	16281-D5.3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWG QGTLVTVSS
51	16281-D5.3 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
52	16281-D5.4 - HCDR1	artificial	KYAIN
53	16281-D5.4 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
54	16281-D5.4 - HCDR3	artificial	AGNFGTSYISYFAY
55	16281-D5.4 - LCDR1	artificial	GSSTGAVTSGNYPN
56	16281-D5.4 - LCDR2	artificial	GTKFLAP
57	16281-D5.4 - LCDR3	artificial	ALWYSNRWV
58	16281-D5.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRAGNFGTSYISYFAYWG QGTLVTVSS
59	16281-D5.4 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
60	16334-G10.4 - HCDR1	artificial	KYAMN
61	16334-G10.4 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
62	16334-G10.4 - HCDR3	artificial	AENIGTSYISYWAY
63	16334-G10.4 - LCDR1	artificial	GSSTGAVTSGNYPN
64	16334-G10.4 - LCDR2	artificial	GTKFLAP
65	16334-G10.4 - LCDR3	artificial	VLWYSNRWV
66	16334-G10.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFSKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRAENIGTSYISYWAYWG QGTLVTVSS
67	16334-G10.4 - VL	artificial	QTVVTQEPSTLVSPGGTVMTCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
68	16335-B1.5 - HCDR1	artificial	KYAMN
69	16335-B1.5 - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
70	16335-B1.5 - HCDR3	artificial	AGNFGSSYISYWAY
71	16335-B1.5 - LCDR1	artificial	GSSTGAVTSGNYPN
72	16335-B1.5 - LCDR2	artificial	GTKFLAP
73	16335-B1.5 - LCDR3	artificial	VLWYSNRWV
74	16335-B1.5 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFSKYAMNWWVRQAPGKMEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRAGNFGSSYISYWAYWG QGTLVTVSS
75	16335-B1.5 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
76	16335-B1.9 - HCDR1	artificial	KYAMN
77	16335-B1.9 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
78	16335-B1.9 - HCDR3	artificial	AGNFGTSYISYFAY
79	16335-B1.9 - LCDR1	artificial	GSSTGAVTSGNYPN
80	16335-B1.9 - LCDR2	artificial	GTKFLAP
81	16335-B1.9 - LCDR3	artificial	VLYYSNRWV

82	16335-B1.9 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFSKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWG QGTLVTVSS
83	16335-B1.9 - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
84	16335-C3.4 - HCDR1	artificial	KYAIN
85	16335-C3.4 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
86	16335-C3.4 - HCDR3	artificial	AENIGTSYISYWAY
87	16335-C3.4 - LCDR1	artificial	GSSTGAVTSGNYPN
88	16335-C3.4 - LCDR2	artificial	GTKFLAP
89	16335-C3.4 - LCDR3	artificial	VLWYSNRWV
90	16335-C3.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAINWRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAENIGTSYISYWAYWG QGTLVTVSS
91	16335-C3.4 - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
92	16335-C3.5 - HCDR1	artificial	KYAIN
93	16335-C3.5 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
94	16335-C3.5 - HCDR3	artificial	AGNFGSSYISYWAY
95	16335-C3.5 - LCDR1	artificial	GSSTGAVTSGNYPN
96	16335-C3.5 - LCDR2	artificial	GTKFLAP
97	16335-C3.5 - LCDR3	artificial	VLYYSNRWV
98	16335-C3.5 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAINWRQAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWG QGTLVTVSS
99	16335-C3.5 - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
100	16335-G6.3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRAGNFGSSYISYWAYWG QGTLVTVSS
101	16335-G6.3 - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
102	16335-G6.4 - HCDR1	artificial	KYAMN
103	16335-G6.4 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
104	16335-G6.4 - HCDR3	artificial	NENIGSSYISYWAY
105	16335-G6.4 - LCDR1	artificial	GSSTGAVTSGNYPN
106	16335-G6.4 - LCDR2	artificial	GTKFLAP
107	16335-G6.4 - LCDR3	artificial	VLWYSNRWV
108	16335-G6.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGSSYISYWAYWG QGTLVTVSS
109	16335-G6.4 - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
110	16356-H10.3 - HCDR1	artificial	KYAMN
111	16356-H10.3 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
112	16356-H10.3 - HCDR3	artificial	AGNFGTSYISYWAY
113	16356-H10.3 - LCDR1	artificial	GSSTGAVTSGNYPN
114	16356-H10.3 - LCDR2	artificial	GTKFLAP
115	16356-H10.3 - LCDR3	artificial	VLWYSNRWV
116	16356-H10.3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWG QGTLVTVSS

117	16356-H10.3 - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWIQKKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
118	2B2_Comp1 - HCDR1	artificial	KYAIN
119	2B2_Comp1 - HCDR2	artificial	RIRSKYNNYATYYADQVKD
120	2B2_Comp1 - HCDR3	artificial	HANFGNSYISYWAY
121	2B2_Comp1 - LCDR1	artificial	ASSTGAVTSGNYPN
122	2B2_Comp1 - LCDR2	artificial	GTKFLVP
123	2B2_Comp1 - LCDR3	artificial	TLWYSNRWV
124	2B2_Comp1 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWG QGTLVTVSS
125	2B2_Comp1 - VL	artificial	QTVVTQEPSTLVSPGGTITITCASSTGAVTSGNYPNWWVQKKPGQAPRGLIGGTKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
126	2B2_Comp1_I 2E - HCDR1	artificial	KYAIN
127	2B2_Comp1_I 2E - HCDR2	artificial	RIRSKYNNYATYYADAVKD
128	2B2_Comp1_I 2E - HCDR3	artificial	AANFGSSYISYWAY
129	2B2_Comp1_I 2E - LCDR1	artificial	ASSTGAVTSGNYPN
130	2B2_Comp1_I 2E - LCDR2	artificial	GTKFLVP
131	2B2_Comp1_I 2E - LCDR3	artificial	TLWYSNRWV
132	2B2_Comp1_I 2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAANFGSSYISYWAYWG QGTLVTVSS
133	2B2_Comp1_I 2E - VL	artificial	QTVVTQEPSTLVSPGGTITITCASSTGAVTSGNYPNWWVQKKPGQAPRGLIGGTKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
134	2B2_Comp1_I 2K - HCDR1	artificial	KYAMN
135	2B2_Comp1_I 2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
136	2B2_Comp1_I 2K - HCDR3	artificial	NENIGTSYISYWAY
137	2B2_Comp1_I 2K - LCDR1	artificial	ASSTGAVTSGNYPN
138	2B2_Comp1_I 2K - LCDR2	artificial	GTKFLVP
139	2B2_Comp1_I 2K - LCDR3	artificial	TLWYSNRWV
140	2B2_Comp1_I 2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWG QGTLVTVSS
141	2B2_Comp1_I 2K - VL	artificial	QTVVTQEPSTLVSPGGTITITCASSTGAVTSGNYPNWWVQKKPGQAPRGLIGGTKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
142	2B2_Comp1_I 2L - HCDR1	artificial	KYAIN
143	2B2_Comp1_I 2L - HCDR2	artificial	RIRSKYNNYATYYADAVKD
144	2B2_Comp1_I 2L - HCDR3	artificial	AANFGSSYISYFAY
145	2B2_Comp1_I 2L - LCDR1	artificial	ASSTGAVTSGNYPN
146	2B2_Comp1_I 2L - LCDR2	artificial	GTKFLVP
147	2B2_Comp1_I 2L - LCDR3	artificial	TLYSNRWV
148	2B2_Comp1_I 2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKMEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRANFGSSYISYFAYWG QGTLVTVSS
149	2B2_Comp1_I 2L - VL	artificial	QTVVTQEPSTLVSPGGTITITCASSTGAVTSGNYPNWIQKKPGQAPRGLIGGTKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLYYSNRWVFGSGTKLTVL
150	2B2_Comp1_I 2M - HCDR1	artificial	KYAIN
151	2B2_Comp1_I 2M - HCDR2	artificial	RIRSKYNNYATYYADAVKD
152	2B2_Comp1_I 2M - HCDR3	artificial	AANFGTSYISYWAY

153	2B2_Compl_I 2M - LCDR1	artificial	ASSTGAVTSGNYPN
154	2B2_Compl_I 2M - LCDR2	artificial	GTKFLVP
155	2B2_Compl_I 2M - LCDR3	artificial	TLWYSNRWV
156	2B2_Compl_I 2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGMWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAANFGTSYISYWAYWG QGTLVTVSS
157	2B2_Compl_I 2M - VL	artificial	QTVVTQEPSTLVSPGGTITCASSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
158	2B2_Compl_I 2M2 - HCDR1	artificial	KYAIN
159	2B2_Compl_I 2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
160	2B2_Compl_I 2M2 - HCDR3	artificial	NANFGTSYISYFAY
161	2B2_Compl_I 2M2 - LCDR1	artificial	ASSTGAVTSGNYPN
162	2B2_Compl_I 2M2 - LCDR2	artificial	GTKFLVP
163	2B2_Compl_I 2M2 - LCDR3	artificial	TLWYSNRWV
164	2B2_Compl_I 2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWG QGTLVTVSS
165	2B2_Compl_I 2M2 - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
166	A2J - HCDR1	artificial	VYAMN
167	A2J - HCDR2	artificial	RIRSKYNNYATYYADSVKK
168	A2J - HCDR3	artificial	HGNFGNSYLSWWAY
169	A2J - LCDR1	artificial	RSSTGAVTSGYYPN
170	A2J - LCDR2	artificial	ATDMRPS
171	A2J - LCDR3	artificial	ALWYSNRWV
172	A2J - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYLSWWAYWG QGTLVTVSS
173	A2J - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGYYPNWWVQKKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
174	A2J_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNGNSYLSWWAYWG QGTLVTVSS
175	A2J_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGYYPNWWVQKKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
176	A2J_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNGNSYLSWWAYWG QGTLVTVSS
177	A2J_HC_A89L - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGYYPNWWVQKKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
178	A2J_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTTYLQMNNLKTEDTAVYYCVRHGNGNSYLSWWAYWG QGTLVTVSS
179	A2J_HC_A89T - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGYYPNWWVQKKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
180	A2J_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNGNSYLSWWAYWG QGTLVTVSS
181	A2J_HC_A89V - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGYYPNWWVQKKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
182	A2J_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYLSWWAYWG QGTLVTVSS
183	A2J_HC_L52M - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGYYPNWWVQKKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
184	A2J_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYLSWWAYWG QGTLVTVSS
185	A2J_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITLTCSSTGAVTSGYYPNWWVQKKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

186	A2J_HC_L52M _LC_Q46K - _VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
187	A2J_HC_L52M _LC_Q46K - _VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
188	A2J_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
189	A2J_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
190	A2J_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
191	A2J_HC_L52V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
192	A2J_HC_L52V _LC_V44F - _VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
193	A2J_HC_L52V _LC_V44F - _VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
194	A2J_HC_L52V _LC_V44Y - _VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
195	A2J_HC_L52V _LC_V44Y - _VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
196	A2J_HC_M41F _A89V - HCDR1	artificial	VYAFN
197	A2J_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
198	A2J_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYLSWWAY
199	A2J_HC_M41F _A89V - LCDR1	artificial	RSSTGAVTSGYYPN
200	A2J_HC_M41F _A89V - LCDR2	artificial	ATDMRPS
201	A2J_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
202	A2J_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAFNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
203	A2J_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
204	A2J_HC_M41I - HCDR1	artificial	VYAIN
205	A2J_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKK
206	A2J_HC_M41I - HCDR3	artificial	HGNFGNSYLSWWAY
207	A2J_HC_M41I - LCDR1	artificial	RSSTGAVTSGYYPN
208	A2J_HC_M41I - LCDR2	artificial	ATDMRPS
209	A2J_HC_M41I - LCDR3	artificial	ALWYSNRWV
210	A2J_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
211	A2J_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
212	A2J_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
213	A2J_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
214	A2J_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG

			QGTILVTVSS
215	A2J_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
216	A2J_HC_M41I _A89V LC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
217	A2J_HC_M41I _A89V LC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
218	A2J_HC_M41I _A89V LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
219	A2J_HC_M41I _A89V LC_Q4 6K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
220	A2J_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
221	A2J_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
222	A2J_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
223	A2J_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
224	A2J_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
225	A2J_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
226	A2J_HC_M41V - HCDR1	artificial	VYAVN
227	A2J_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
228	A2J_HC_M41V - HCDR3	artificial	HGNFGNSYLSWWAY
229	A2J_HC_M41V - LCDR1	artificial	RSSTGAVTSGYYPN
230	A2J_HC_M41V - LCDR2	artificial	ATDMRPS
231	A2J_HC_M41V - LCDR3	artificial	ALWYSNRWV
232	A2J_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
233	A2J_HC_M41V - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
234	A2J_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
235	A2J_HC_Q46D - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
236	A2J_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTILVTVSS
237	A2J_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

238	A2J_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
239	A2J_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQRKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
240	A2J_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
241	A2J_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
242	A2J_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
243	A2J_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
244	A2J_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
245	A2J_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQRKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
246	A2J_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
247	A2J_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQRKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
248	A2J_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
249	A2J_HC_Q46E - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
250	A2J_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
251	A2J_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
252	A2J_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
253	A2J_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQRKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
254	A2J_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
255	A2J_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
256	A2J_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
257	A2J_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
258	A2J_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
259	A2J_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQRKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
260	A2J_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
261	A2J_HC_Q46E _LC_Q46R_G1	artificial	QTVVTQEPSLTVSPGGTITICRSSTGAVTSGYYPNWVQRKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

	41S - VL		
262	A2J_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
263	A2J_HC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
264	A2J_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
265	A2J_HC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
266	A2J_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYLSWWAYWG QGTLVTVSS
267	A2J_HC_V107 A - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
268	A2J_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYLSWWAYWG QGTLVTVSS
269	A2J_HC_V107 L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
270	A2J_HC_W136 F - HCDR1	artificial	VYAMN
271	A2J_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKK
272	A2J_HC_W136 F - HCDR3	artificial	HGNFGNSYLSWFAY
273	A2J_HC_W136 F - LCDR1	artificial	RSSTGAVTSGYYPN
274	A2J_HC_W136 F - LCDR2	artificial	ATDMRPS
275	A2J_HC_W136 F - LCDR3	artificial	ALWYSNRWV
276	A2J_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWFAYWG QGTLVTVSS
277	A2J_HC_W136 F - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
278	A2J_HC_W136 F_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWFAYWG QGTLVTVSS
279	A2J_HC_W136 F_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
280	A2J_HC_W136 F_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWFAYWG QGTLVTVSS
281	A2J_HC_W136 F_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
282	A2J_I2E - HCDR1	artificial	VYAIN
283	A2J_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKK
284	A2J_I2E - HCDR3	artificial	AGNFGSSYLSWWAY
285	A2J_I2E - LCDR1	artificial	RSSTGAVTSGYYPN
286	A2J_I2E - LCDR2	artificial	ATDMRPS
287	A2J_I2E - LCDR3	artificial	ALWYSNRWV
288	A2J_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWRKAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYLSWWAYWG QGTLVTVSS
289	A2J_I2E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
290	A2J_I2K - HCDR1	artificial	VYAMN
291	A2J_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
292	A2J_I2K - HCDR3	artificial	NENIGTSYLSWWAY
293	A2J_I2K - LCDR1	artificial	RSSTGAVTSGYYPN

294	A2J_I2K - LCDR2	artificial	ATDMRPS
295	A2J_I2K - LCDR3	artificial	ALWYSNRWV
296	A2J_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYLSWWAYWG QGTLVTVSS
297	A2J_I2K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
298	A2J_I2L - HCDR1	artificial	VYAMN
299	A2J_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKK
300	A2J_I2L - HCDR3	artificial	AGNFGSSYLSWFAY
301	A2J_I2L - LCDR1	artificial	RSSTGAVTSGYYPN
302	A2J_I2L - LCDR2	artificial	ATDMRPS
303	A2J_I2L - LCDR3	artificial	ALYYSNRWV
304	A2J_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKMEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYLSWFAYWG QGTLVTVSS
305	A2J_I2L - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWIQKPGQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
306	A2J_I2M - HCDR1	artificial	VYAMN
307	A2J_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKK
308	A2J_I2M - HCDR3	artificial	AGNFGTSYLSWWAY
309	A2J_I2M - LCDR1	artificial	RSSTGAVTSGYYPN
310	A2J_I2M - LCDR2	artificial	ATDMRPS
311	A2J_I2M - LCDR3	artificial	ALWYSNRWV
312	A2J_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKMEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYLSWWAYWG QGTLVTVSS
313	A2J_I2M - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
314	A2J_I2M2 - HCDR1	artificial	VYAIN
315	A2J_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKK
316	A2J_I2M2 - HCDR3	artificial	NANFGTSYLSWFAY
317	A2J_I2M2 - LCDR1	artificial	RSSTGAVTSGYYPN
318	A2J_I2M2 - LCDR2	artificial	ATDMRPS
319	A2J_I2M2 - LCDR3	artificial	ALWYSNRWV
320	A2J_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYLSWFAYWG QGTLVTVSS
321	A2J_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
322	A2J_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
323	A2J_LC_G141 S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
324	A2J_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
325	A2J_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
326	A2J_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
327	A2J_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL

328	A2J_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
329	A2J_LC_L83S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
330	A2J_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
331	A2J_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
332	A2J_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
333	A2J_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
334	A2J_LC_A107 L - HCDR1	artificial	VYAMN
335	A2J_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKK
336	A2J_LC_A107 L - HCDR3	artificial	HGNFGNSYLSWWAY
337	A2J_LC_A107 L - LCDR1	artificial	RSSTGAVTSGYYPN
338	A2J_LC_A107 L - LCDR2	artificial	ATDMRPS
339	A2J_LC_A107 L - LCDR3	artificial	LLWYSNRWV
340	A2J_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
341	A2J_LC_A107 L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCLWYSNRWVFGGGTKLTVL
342	A2J_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
343	A2J_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
344	A2J_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
345	A2J_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
346	A2J_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
347	A2J_LC_V44M - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
348	A2J_LC_W109 Y - HCDR1	artificial	VYAMN
349	A2J_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKK
350	A2J_LC_W109 Y - HCDR3	artificial	HGNFGNSYLSWWAY
351	A2J_LC_W109 Y - LCDR1	artificial	RSSTGAVTSGYYPN
352	A2J_LC_W109 Y - LCDR2	artificial	ATDMRPS
353	A2J_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
354	A2J_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
355	A2J_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
356	E1L - HCDR1	artificial	KYAMN
357	E1L - HCDR2	artificial	RIRSKYNNYATYYADSVKS
358	E1L - HCDR3	artificial	HGNFGNSYTSYYAY
359	E1L - LCDR1	artificial	GSSTGAVTSGYYPN
360	E1L - LCDR2	artificial	GTKFLAP
361	E1L - LCDR3	artificial	ALWYSNRWV
362	E1L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG

			QGTILVTVSS
363	ElL - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
364	ElL_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
365	ElL_HC_A89I - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
366	ElL_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
367	ElL_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
368	ElL_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
369	ElL_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
370	ElL_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
371	ElL_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
372	ElL_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
373	ElL_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
374	ElL_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
375	ElL_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
376	ElL_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
377	ElL_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
378	ElL_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
379	ElL_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
380	ElL_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
381	ElL_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
382	ElL_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
383	ElL_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
384	ElL_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTILVTVSS
385	ElL_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
386	ElL_HC_M41F _A89V - HCDR1	artificial	KYAFN
387	ElL_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
388	ElL_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYTSYYAY
389	ElL_HC_M41F _A89V -	artificial	GSSTGAVTSGYYPN

	LCDR1		
390	E1L_HC_M41F_A89V - LCDR2	artificial	GTKFLAP
391	E1L_HC_M41F_A89V - LCDR3	artificial	ALWYSNRWV
392	E1L_HC_M41F_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAFNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
393	E1L_HC_M41F_A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
394	E1L_HC_M41I - HCDR1	artificial	KYAIN
395	E1L_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKS
396	E1L_HC_M41I - HCDR3	artificial	HGNFGNSYTSYYAY
397	E1L_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
398	E1L_HC_M41I - LCDR2	artificial	GTKFLAP
399	E1L_HC_M41I - LCDR3	artificial	ALWYSNRWV
400	E1L_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
401	E1L_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
402	E1L_HC_M41I_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
403	E1L_HC_M41I_A89L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
404	E1L_HC_M41I_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
405	E1L_HC_M41I_A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
406	E1L_HC_M41I_A89V_LC_L2_1I_Q46K_G14_1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
407	E1L_HC_M41I_A89V_LC_L2_1I_Q46K_G14_1S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
408	E1L_HC_M41I_A89V_LC_Q4_6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
409	E1L_HC_M41I_A89V_LC_Q4_6K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
410	E1L_HC_M41I_L52V_A89V_LC_L21I_Q46_K_G141S_V44_F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
411	E1L_HC_M41I_L52V_A89V_LC_L21I_Q46_K_G141S_V44_F - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
412	E1L_HC_M41I_LC_L21I_Q4_6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
413	E1L_HC_M41I_LC_L21I_Q4_6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
414	E1L_HC_M41I_Q46E_A89V_LC_L21I_Q46_K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS

415	E1L_HC_M41I _Q46E_A89V _LC_L21I_Q46 _K_G141S - _VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
416	E1L_HC_M41V - HCDR1	artificial	KYAVN
417	E1L_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
418	E1L_HC_M41V - HCDR3	artificial	HGNFGNSYTSYYAY
419	E1L_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
420	E1L_HC_M41V - LCDR2	artificial	GTKFLAP
421	E1L_HC_M41V - LCDR3	artificial	ALWYSNRWV
422	E1L_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
423	E1L_HC_M41V - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
424	E1L_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
425	E1L_HC_Q46D - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
426	E1L_HC_Q46D _LC_L21I_Q4 _6K_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
427	E1L_HC_Q46D _LC_L21I_Q4 _6K_G141S - _VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
428	E1L_HC_Q46D _LC_L21I_Q4 _6R_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
429	E1L_HC_Q46D _LC_L21I_Q4 _6R_G141S - _VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
430	E1L_HC_Q46D _LC_Q46K - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
431	E1L_HC_Q46D _LC_Q46K - _VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
432	E1L_HC_Q46D _LC_Q46K_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
433	E1L_HC_Q46D _LC_Q46K_G1 _41S - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
434	E1L_HC_Q46D _LC_Q46R - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
435	E1L_HC_Q46D _LC_Q46R - _VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
436	E1L_HC_Q46D _LC_Q46R_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
437	E1L_HC_Q46D _LC_Q46R_G1 _41S - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
438	E1L_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
439	E1L_HC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
440	E1L_HC_Q46E _LC_L21I_Q4 _6K_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS

441	E1L_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
442	E1L_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
443	E1L_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
444	E1L_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
445	E1L_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
446	E1L_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
447	E1L_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
448	E1L_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
449	E1L_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
450	E1L_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
451	E1L_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
452	E1L_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
453	E1L_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
454	E1L_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
455	E1L_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
456	E1L_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYTSYYAYWG QGTLVTVSS
457	E1L_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
458	E1L_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYTSYYAYWG QGTLVTVSS
459	E1L_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
460	E1L_HC_Y136 F - HCDR1	artificial	KYAMN
461	E1L_HC_Y136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKS
462	E1L_HC_Y136 F - HCDR3	artificial	HGNFGNSYTSYFAY
463	E1L_HC_Y136 F - LCDR1	artificial	GSSTGAVTSGYYPN
464	E1L_HC_Y136 F - LCDR2	artificial	GTKFLAP
465	E1L_HC_Y136 F - LCDR3	artificial	ALWYSNRWV
466	E1L_HC_Y136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYFAYWG QGTLVTVSS
467	E1L_HC_Y136 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
468	E1L_HC_Y136 F_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYFAYWG QGTLVTVSS

469	E1L_HC_Y136 F LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWIQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
470	E1L_HC_Y136 F LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYFAYWG QGTLVTVSS
471	E1L_HC_Y136 F LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWLQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
472	E1L_I2E - HCDR1	artificial	KYAIN
473	E1L_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKS
474	E1L_I2E - HCDR3	artificial	AGNFGSSYTSYYAY
475	E1L_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
476	E1L_I2E - LCDR2	artificial	GTKFLAP
477	E1L_I2E - LCDR3	artificial	ALWYSNRWV
478	E1L_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYTSYYAYWG QGTLVTVSS
479	E1L_I2E - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
480	E1L_I2K - HCDR1	artificial	KYAMN
481	E1L_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
482	E1L_I2K - HCDR3	artificial	NENIGTSYTSYYAY
483	E1L_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
484	E1L_I2K - LCDR2	artificial	GTKFLAP
485	E1L_I2K - LCDR3	artificial	ALWYSNRWV
486	E1L_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYTSYYAYWG QGTLVTVSS
487	E1L_I2K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
488	E1L_I2L - HCDR1	artificial	KYAMN
489	E1L_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKS
490	E1L_I2L - HCDR3	artificial	AGNFGSSYTSYFAY
491	E1L_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
492	E1L_I2L - LCDR2	artificial	GTKFLAP
493	E1L_I2L - LCDR3	artificial	ALYYSNRWV
494	E1L_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYTSYFAYWG QGTLVTVSS
495	E1L_I2L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWIQKPGQAPRGLIGGTFKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
496	E1L_I2M - HCDR1	artificial	KYAMN
497	E1L_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKS
498	E1L_I2M - HCDR3	artificial	AGNFGTSYTSYYAY
499	E1L_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
500	E1L_I2M - LCDR2	artificial	GTKFLAP
501	E1L_I2M - LCDR3	artificial	ALWYSNRWV
502	E1L_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYTSYYAYWG QGTLVTVSS

503	E1L_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
504	E1L_I2M2 - HCDR1	artificial	KYAIN
505	E1L_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKS
506	E1L_I2M2 - HCDR3	artificial	NANFGTSYTSYFAY
507	E1L_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
508	E1L_I2M2 - LCDR2	artificial	GTKFLAP
509	E1L_I2M2 - LCDR3	artificial	ALWYSNRWV
510	E1L_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRNANFGTSYTSYFAYWG QGTLVTVSS
511	E1L_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
512	E1L_LC_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
513	E1L_LC_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
514	E1L_LC_G141S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
515	E1L_LC_G141S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
516	E1L_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
517	E1L_LC_L83E - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
518	E1L_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
519	E1L_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
520	E1L_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
521	E1L_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
522	E1L_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
523	E1L_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
524	E1L_LC_A107L - HCDR1	artificial	KYAMN
525	E1L_LC_A107L - HCDR2	artificial	RIRSKYNNYATYYADSVKS
526	E1L_LC_A107L - HCDR3	artificial	HGNFGNSYTSYYAY
527	E1L_LC_A107L - LCDR1	artificial	GSSTGAVTSGYYPN
528	E1L_LC_A107L - LCDR2	artificial	GTKFLAP
529	E1L_LC_A107L - LCDR3	artificial	LLWYSNRWV
530	E1L_LC_A107L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
531	E1L_LC_A107L - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
532	E1L_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
533	E1L_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
534	E1L_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
535	E1L_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

536	E1L_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYTSYYAYWG QGTLVTVSS
537	E1L_LC_V44M - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
538	E1L_LC_W109 Y - HCDR1	artificial	KYAMN
539	E1L_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKS
540	E1L_LC_W109 Y - HCDR3	artificial	HGNFGNSYTSYYAY
541	E1L_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
542	E1L_LC_W109 Y - LCDR2	artificial	GTKFLAP
543	E1L_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
544	E1L_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYTSYYAYWG QGTLVTVSS
545	E1L_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
546	E2M - HCDR1	artificial	GYAMN
547	E2M - HCDR2	artificial	RIRSKYNNYATYYADSVKE
548	E2M - HCDR3	artificial	HRNFGNSYLSWFAY
549	E2M - LCDR1	artificial	RSSTGAVTSGYYPN
550	E2M - LCDR2	artificial	ATDMRPS
551	E2M - LCDR3	artificial	ALWYSNRWV
552	E2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
553	E2M - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
554	E2M_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
555	E2M_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
556	E2M_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
557	E2M_HC_A89L - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
558	E2M_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
559	E2M_HC_A89T - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
560	E2M_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
561	E2M_HC_A89V - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
562	E2M_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
563	E2M_HC_L52M - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
564	E2M_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
565	E2M_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
566	E2M_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
567	E2M_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

568	E2M_HC_L52M LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
569	E2M_HC_L52M LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
570	E2M_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
571	E2M_HC_L52V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
572	E2M_HC_L52V LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
573	E2M_HC_L52V LC_V44F - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
574	E2M_HC_L52V LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
575	E2M_HC_L52V LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
576	E2M_HC_M41F _A89V - HCDR1	artificial	GYAFN
577	E2M_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKE
578	E2M_HC_M41F _A89V - HCDR3	artificial	HRNFGNSYLSWFAY
579	E2M_HC_M41F _A89V - LCDR1	artificial	RSSTGAVTSGYYPN
580	E2M_HC_M41F _A89V - LCDR2	artificial	ATDMRPS
581	E2M_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
582	E2M_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
583	E2M_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
584	E2M_HC_M41I - HCDR1	artificial	GYAIN
585	E2M_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKE
586	E2M_HC_M41I - HCDR3	artificial	HRNFGNSYLSWFAY
587	E2M_HC_M41I - LCDR1	artificial	RSSTGAVTSGYYPN
588	E2M_HC_M41I - LCDR2	artificial	ATDMRPS
589	E2M_HC_M41I - LCDR3	artificial	ALWYSNRWV
590	E2M_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
591	E2M_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
592	E2M_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
593	E2M_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
594	E2M_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
595	E2M_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
596	E2M_HC_M41I _A89V LC_L2 1I_Q46K_G14	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS

	1S - VH		
597	E2M_HC_M41I _A89V_LC_L2 _L1_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
598	E2M_HC_M41I _A89V_LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
599	E2M_HC_M41I _A89V_LC_Q4 6K - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
600	E2M_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
601	E2M_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
602	E2M_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
603	E2M_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
604	E2M_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
605	E2M_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
606	E2M_HC_M41V - HCDR1	artificial	GYAVN
607	E2M_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKE
608	E2M_HC_M41V - HCDR3	artificial	HRNFGNSYLSWFAY
609	E2M_HC_M41V - LCDR1	artificial	RSSTGAVTSGYYPN
610	E2M_HC_M41V - LCDR2	artificial	ATDMRPS
611	E2M_HC_M41V - LCDR3	artificial	ALWYSNRWV
612	E2M_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
613	E2M_HC_M41V - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
614	E2M_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
615	E2M_HC_Q46D - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
616	E2M_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
617	E2M_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
618	E2M_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
619	E2M_HC_Q46D _LC_L21I_Q4 6R_G141S -	artificial	QTVVTQEPSTLVSPGGTITICRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

	VL		
620	E2M_HC_Q46D _LC_Q46K - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
621	E2M_HC_Q46D _LC_Q46K - _VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
622	E2M_HC_Q46D _LC_Q46K_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
623	E2M_HC_Q46D _LC_Q46K_G1 _41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
624	E2M_HC_Q46D _LC_Q46R - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
625	E2M_HC_Q46D _LC_Q46R - _VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
626	E2M_HC_Q46D _LC_Q46R_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
627	E2M_HC_Q46D _LC_Q46R_G1 _41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
628	E2M_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
629	E2M_HC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
630	E2M_HC_Q46E _LC_L21I_Q4 _6K_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
631	E2M_HC_Q46E _LC_L21I_Q4 _6K_G141S - _VL	artificial	QTVVTQEPSTLVSPGGTVTITCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
632	E2M_HC_Q46E _LC_L21I_Q4 _6R_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
633	E2M_HC_Q46E _LC_L21I_Q4 _6R_G141S - _VL	artificial	QTVVTQEPSTLVSPGGTVTITCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
634	E2M_HC_Q46E _LC_Q46K - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
635	E2M_HC_Q46E _LC_Q46K - _VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
636	E2M_HC_Q46E _LC_Q46K_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
637	E2M_HC_Q46E _LC_Q46K_G1 _41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
638	E2M_HC_Q46E _LC_Q46R - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
639	E2M_HC_Q46E _LC_Q46R - _VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
640	E2M_HC_Q46E _LC_Q46R_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
641	E2M_HC_Q46E _LC_Q46R_G1 _41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
642	E2M_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
643	E2M_HC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

644	E2M_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
645	E2M_HC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
646	E2M_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHRNFNGSYLSWFAYWG QGTLVTVSS
647	E2M_HC_V107 A - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
648	E2M_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRRHNFNGSYLSWFAYWG QGTLVTVSS
649	E2M_HC_V107 L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
650	E2M_I2E - HCDR1	artificial	GYAIN
651	E2M_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKE
652	E2M_I2E - HCDR3	artificial	ARNFGSSYLSWFAY
653	E2M_I2E - LCDR1	artificial	RSSTGAVTSGYYPN
654	E2M_I2E - LCDR2	artificial	ATDMRPS
655	E2M_I2E - LCDR3	artificial	ALWYSNRWV
656	E2M_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCARARNFGSSYLSWFAYWG QGTLVTVSS
657	E2M_I2E - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
658	E2M_I2K - HCDR1	artificial	GYAMN
659	E2M_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
660	E2M_I2K - HCDR3	artificial	NENIGTSYLSWFAY
661	E2M_I2K - LCDR1	artificial	RSSTGAVTSGYYPN
662	E2M_I2K - LCDR2	artificial	ATDMRPS
663	E2M_I2K - LCDR3	artificial	ALWYSNRWV
664	E2M_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRRNENIGTSYLSWFAYWG QGTLVTVSS
665	E2M_I2K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
666	E2M_I2L - HCDR1	artificial	GYAMN
667	E2M_I2L - HCDR2	artificial	RIRSKYNNYATYYAEAVKE
668	E2M_I2L - HCDR3	artificial	ARNFGSSYLSWFAY
669	E2M_I2L - LCDR1	artificial	RSSTGAVTSGYYPN
670	E2M_I2L - LCDR2	artificial	ATDMRPS
671	E2M_I2L - LCDR3	artificial	ALYYSNRWV
672	E2M_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRRARNFGSSYLSWFAYWG QGTLVTVSS
673	E2M_I2L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
674	E2M_I2M - HCDR1	artificial	GYAMN
675	E2M_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKE
676	E2M_I2M - HCDR3	artificial	ARNFGTSYLSWFAY
677	E2M_I2M - LCDR1	artificial	RSSTGAVTSGYYPN
678	E2M_I2M - LCDR2	artificial	ATDMRPS

679	E2M_I2M - LCDR3	artificial	ALWYSNRWV
680	E2M_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRRNRFNGTSYLSWFAYWG QGTLVTVSS
681	E2M_I2M - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
682	E2M_I2M2 - HCDR1	artificial	GYAIN
683	E2M_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKE
684	E2M_I2M2 - HCDR3	artificial	NANFGTSYLSFFAY
685	E2M_I2M2 - LCDR1	artificial	RSSTGAVTSGYYPN
686	E2M_I2M2 - LCDR2	artificial	ATDMRPS
687	E2M_I2M2 - LCDR3	artificial	ALWYSNRWV
688	E2M_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRNRFNGTSYLSYFAYWG QGTLVTVSS
689	E2M_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
690	E2M_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
691	E2M_LC_G141 S - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
692	E2M_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
693	E2M_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
694	E2M_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
695	E2M_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
696	E2M_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
697	E2M_LC_L83S - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
698	E2M_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
699	E2M_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
700	E2M_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
701	E2M_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
702	E2M_LC_A107 L - HCDR1	artificial	GYAMN
703	E2M_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKE
704	E2M_LC_A107 L - HCDR3	artificial	HRNFGNSYLSWFAY
705	E2M_LC_A107 L - LCDR1	artificial	RSSTGAVTSGYYPN
706	E2M_LC_A107 L - LCDR2	artificial	ATDMRPS
707	E2M_LC_A107 L - LCDR3	artificial	LLWYSNRWV
708	E2M_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
709	E2M_LC_A107 L - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
710	E2M_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRRHNFNGSYLSWFAYWG QGTLVTVSS
711	E2M_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTITITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

712	E2M_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
713	E2M_LC_V44L - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSRSTGAVTSGYYPNWLQQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
714	E2M_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
715	E2M_LC_V44M - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSRSTGAVTSGYYPNWMMQQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
716	E2M_LC_W109 Y - HCDR1	artificial	GYAMN
717	E2M_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKE
718	E2M_LC_W109 Y - HCDR3	artificial	HRNFGNSYLSWFAY
719	E2M_LC_W109 Y - LCDR1	artificial	RSSTGAVTSGYYPN
720	E2M_LC_W109 Y - LCDR2	artificial	ATDMRPS
721	E2M_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
722	E2M_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
723	E2M_LC_W109 Y - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
724	F12Q - HCDR1	artificial	SYAMN
725	F12Q - HCDR2	artificial	RIRSKYNNYATYYADSVKG
726	F12Q - HCDR3	artificial	HGNFGNSYVSWWAY
727	F12Q - LCDR1	artificial	GSSTGAVTSGNYPN
728	F12Q - LCDR2	artificial	GTKFLAP
729	F12Q - LCDR3	artificial	VLWYSNRWV
730	F12Q - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
731	F12Q - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
732	F12Q_HC_A89 I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
733	F12Q_HC_A89 I - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
734	F12Q_HC_A89 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
735	F12Q_HC_A89 L - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
736	F12Q_HC_A89 T - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTTYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
737	F12Q_HC_A89 T - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
738	F12Q_HC_A89 V - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
739	F12Q_HC_A89 V - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
740	F12Q_HC_L52 M - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
741	F12Q_HC_L52 M - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
742	F12Q_HC_L52 M_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
743	F12Q_HC_L52 M_LC_L21I_Q 46K_G141S -	artificial	QTVVTQEPSLTVSPGGTVTITCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

	VL		
744	F12Q_HC_L52 M_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
745	F12Q_HC_L52 M_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
746	F12Q_HC_L52 M_LC_Q46K_G L41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
747	F12Q_HC_L52 M_LC_Q46K_G L41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
748	F12Q_HC_L52 V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
749	F12Q_HC_L52 V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
750	F12Q_HC_L52 V_LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
751	F12Q_HC_L52 V_LC_V44F - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
752	F12Q_HC_L52 V_LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
753	F12Q_HC_L52 V_LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
754	F12Q_HC_M41 F_A89V - HCDR1	artificial	SYAFN
755	F12Q_HC_M41 F_A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
756	F12Q_HC_M41 F_A89V - HCDR3	artificial	HGNFGNSYVSWWAY
757	F12Q_HC_M41 F_A89V - LCDR1	artificial	GSSTGAVTSGNYPN
758	F12Q_HC_M41 F_A89V - LCDR2	artificial	GTKFLAP
759	F12Q_HC_M41 F_A89V - LCDR3	artificial	VLWYSNRWV
760	F12Q_HC_M41 F_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAFNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
761	F12Q_HC_M41 F_A89V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
762	F12Q_HC_M41 I - HCDR1	artificial	SYAIN
763	F12Q_HC_M41 I - HCDR2	artificial	RIRSKYNNYATYYADSVKG
764	F12Q_HC_M41 I - HCDR3	artificial	HGNFGNSYVSWWAY
765	F12Q_HC_M41 I - LCDR1	artificial	GSSTGAVTSGNYPN
766	F12Q_HC_M41 I - LCDR2	artificial	GTKFLAP
767	F12Q_HC_M41 I - LCDR3	artificial	VLWYSNRWV
768	F12Q_HC_M41 I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
769	F12Q_HC_M41 I - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
770	F12Q_HC_M41 I_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
771	F12Q_HC_M41 I_A89L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

772	F12Q_HC_M41 I_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
773	F12Q_HC_M41 I_A89V - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTCLTVL
774	F12Q_HC_M41 I_A89V_IC_L 21I_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
775	F12Q_HC_M41 I_A89V_IC_L 21I_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
776	F12Q_HC_M41 I_A89V_IC_Q 46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
777	F12Q_HC_M41 I_A89V_IC_Q 46K - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTCLTVL
778	F12Q_HC_M41 I_L52V_A89V LC_L21I_Q4 6K_G141S_V4 4F - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
779	F12Q_HC_M41 I_L52V_A89V LC_L21I_Q4 6K_G141S_V4 4F - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
780	F12Q_HC_M41 I_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
781	F12Q_HC_M41 I_LC_L21I_Q 46K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
782	F12Q_HC_M41 I_Q46E_A89V LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
783	F12Q_HC_M41 I_Q46E_A89V LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
784	F12Q_HC_M41 V - HCDR1	artificial	SYAVN
785	F12Q_HC_M41 V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
786	F12Q_HC_M41 V - HCDR3	artificial	HGNFGNSYVSWWAY
787	F12Q_HC_M41 V - LCDR1	artificial	GSSTGAVTSGNYPN
788	F12Q_HC_M41 V - LCDR2	artificial	GTKFLAP
789	F12Q_HC_M41 V - LCDR3	artificial	VLWYSNRWV
790	F12Q_HC_M41 V - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
791	F12Q_HC_M41 V - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTCLTVL
792	F12Q_HC_Q46 D - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
793	F12Q_HC_Q46 D - VL	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTCLTVL
794	F12Q_HC_Q46 D_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
795	F12Q_HC_Q46 D_LC_L21I_Q 46K_G141S -	artificial	QTVVTQEPSLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

	VL		
796	F12Q_HC_Q46 D_LC_L21I_Q 46R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
797	F12Q_HC_Q46 D_LC_L21I_Q 46R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
798	F12Q_HC_Q46 D_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
799	F12Q_HC_Q46 D_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
800	F12Q_HC_Q46 D_LC_Q46K_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
801	F12Q_HC_Q46 D_LC_Q46K_G 141S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
802	F12Q_HC_Q46 D_LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
803	F12Q_HC_Q46 D_LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
804	F12Q_HC_Q46 D_LC_Q46R_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
805	F12Q_HC_Q46 D_LC_Q46R_G 141S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
806	F12Q_HC_Q46 E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
807	F12Q_HC_Q46 E - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
808	F12Q_HC_Q46 E_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
809	F12Q_HC_Q46 E_LC_L21I_Q 46K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
810	F12Q_HC_Q46 E_LC_L21I_Q 46R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
811	F12Q_HC_Q46 E_LC_L21I_Q 46R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
812	F12Q_HC_Q46 E_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
813	F12Q_HC_Q46 E_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
814	F12Q_HC_Q46 E_LC_Q46K_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
815	F12Q_HC_Q46 E_LC_Q46K_G 141S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
816	F12Q_HC_Q46 E_LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
817	F12Q_HC_Q46 E_LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
818	F12Q_HC_Q46 E_LC_Q46R_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS

819	F12Q_HC_Q46 E LC_Q46R_G 141S - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
820	F12Q_HC_Q46 K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRKAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
821	F12Q_HC_Q46 K - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
822	F12Q_HC_Q46 R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRRAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWG QGTLVTVSS
823	F12Q_HC_Q46 R - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
824	F12Q_HC_V10 7A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHNGFNSYVSWWAYWG QGTLVTVSS
825	F12Q_HC_V10 7A - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
826	F12Q_HC_V10 7L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNGFNSYVSWWAYWG QGTLVTVSS
827	F12Q_HC_V10 7L - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
828	F12Q_HC_W13 6F - HCDR1	artificial	SYAMN
829	F12Q_HC_W13 6F - HCDR2	artificial	RIRSKYNNYATYYADSVKG
830	F12Q_HC_W13 6F - HCDR3	artificial	HGNFGNSYVSWFAY
831	F12Q_HC_W13 6F - LCDR1	artificial	GSSTGAVTSGNYPN
832	F12Q_HC_W13 6F - LCDR2	artificial	GTKFLAP
833	F12Q_HC_W13 6F - LCDR3	artificial	VLWYSNRWV
834	F12Q_HC_W13 6F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWFAYWG QGTLVTVSS
835	F12Q_HC_W13 6F - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
836	F12Q_HC_W13 6F LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWFAYWG QGTLVTVSS
837	F12Q_HC_W13 6F LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
838	F12Q_HC_W13 6F LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWFAYWG QGTLVTVSS
839	F12Q_HC_W13 6F LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWLQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
840	F12Q_I2E - HCDR1	artificial	SYAIN
841	F12Q_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKG
842	F12Q_I2E - HCDR3	artificial	AGNFGSSYVSWWAY
843	F12Q_I2E - LCDR1	artificial	GSSTGAVTSGNYPN
844	F12Q_I2E - LCDR2	artificial	GTKFLAP
845	F12Q_I2E - LCDR3	artificial	VLWYSNRWV
846	F12Q_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYVSWWAYWG QGTLVTVSS
847	F12Q_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
848	F12Q_I2K - HCDR1	artificial	SYAMN
849	F12Q_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
850	F12Q_I2K - HCDR3	artificial	NENIGTSYVSWWAY

851	F12Q_I2K - LCDR1	artificial	GSSTGAVTSGNYPN
852	F12Q_I2K - LCDR2	artificial	GTKFLAP
853	F12Q_I2K - LCDR3	artificial	VLWYSNRWV
854	F12Q_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYVSWWAYWG QGTLVTVSS
855	F12Q_I2K - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
856	F12Q_I2L - HCDR1	artificial	SYAMN
857	F12Q_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKG
858	F12Q_I2L - HCDR3	artificial	AGNFGSSYVSWFAY
859	F12Q_I2L - LCDR1	artificial	GSSTGAVTSGNYPN
860	F12Q_I2L - LCDR2	artificial	GTKFLAP
861	F12Q_I2L - LCDR3	artificial	VLYYSNRWV
862	F12Q_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYVSWFAYWG QGTLVTVSS
863	F12Q_I2L - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
864	F12Q_I2M - HCDR1	artificial	SYAMN
865	F12Q_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKG
866	F12Q_I2M - HCDR3	artificial	AGNFGTSYVSWWAY
867	F12Q_I2M - LCDR1	artificial	GSSTGAVTSGNYPN
868	F12Q_I2M - LCDR2	artificial	GTKFLAP
869	F12Q_I2M - LCDR3	artificial	VLWYSNRWV
870	F12Q_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYVSWWAYWG QGTLVTVSS
871	F12Q_I2M - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
872	F12Q_I2M2 - HCDR1	artificial	SYAIN
873	F12Q_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
874	F12Q_I2M2 - HCDR3	artificial	NANFGTSYVSWFAY
875	F12Q_I2M2 - LCDR1	artificial	GSSTGAVTSGNYPN
876	F12Q_I2M2 - LCDR2	artificial	GTKFLAP
877	F12Q_I2M2 - LCDR3	artificial	VLWYSNRWV
878	F12Q_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYVSWFAYWG QGTLVTVSS
879	F12Q_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
880	F12Q_LC_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
881	F12Q_LC_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
882	F12Q_LC_G14 1S_I21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
883	F12Q_LC_G14 1S_I21I - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
884	F12Q_LC_L83 E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS

885	F12Q_LC_L83 E - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
886	F12Q_LC_L83 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
887	F12Q_LC_L83 S - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
888	F12Q_LC_Q46 E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
889	F12Q_LC_Q46 E - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
890	F12Q_LC_Q46 K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
891	F12Q_LC_Q46 K - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
892	F12Q_LC_V10 7A - HCDR1	artificial	SYAMN
893	F12Q_LC_V10 7A - HCDR2	artificial	RIRSKYNNYATYYADSVKG
894	F12Q_LC_V10 7A - HCDR3	artificial	HGNFGNSYVSWWAY
895	F12Q_LC_V10 7A - LCDR1	artificial	GSSTGAVTSGNYPN
896	F12Q_LC_V10 7A - LCDR2	artificial	GTKFLAP
897	F12Q_LC_V10 7A - LCDR3	artificial	ALWYSNRWV
898	F12Q_LC_V10 7A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
899	F12Q_LC_V10 7A - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
900	F12Q_LC_V10 7L - HCDR1	artificial	SYAMN
901	F12Q_LC_V10 7L - HCDR2	artificial	RIRSKYNNYATYYADSVKG
902	F12Q_LC_V10 7L - HCDR3	artificial	HGNFGNSYVSWWAY
903	F12Q_LC_V10 7L - LCDR1	artificial	GSSTGAVTSGNYPN
904	F12Q_LC_V10 7L - LCDR2	artificial	GTKFLAP
905	F12Q_LC_V10 7L - LCDR3	artificial	LLWYSNRWV
906	F12Q_LC_V10 7L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
907	F12Q_LC_V10 7L - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
908	F12Q_LC_V44 I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
909	F12Q_LC_V44 I - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
910	F12Q_LC_V44 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
911	F12Q_LC_V44 L - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
912	F12Q_LC_V44 M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
913	F12Q_LC_V44 M - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
914	F12Q_LC_W10 9Y - HCDR1	artificial	SYAMN
915	F12Q_LC_W10 9Y - HCDR2	artificial	RIRSKYNNYATYYADSVKG
916	F12Q_LC_W10 9Y - HCDR3	artificial	HGNFGNSYVSWWAY
917	F12Q_LC_W10 9Y - LCDR1	artificial	GSSTGAVTSGNYPN
918	F12Q_LC_W10 9Y - LCDR2	artificial	GTKFLAP

919	F12Q_LC_W10 9Y - LCDR3	artificial	VLYYSNRWV
920	F12Q_LC_W10 9Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
921	F12Q_LC_W10 9Y - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGGGTKLTVL
922	F6A - HCDR1	artificial	IYAMN
923	F6A - HCDR2	artificial	RIRSKYNNYATYYADSVKS
924	F6A - HCDR3	artificial	HGNFGNSYVSFFAY
925	F6A - LCDR1	artificial	GSSTGAVTSGYYPN
926	F6A - LCDR2	artificial	GTKFLAP
927	F6A - LCDR3	artificial	ALWYSNRWV
928	F6A - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
929	F6A - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
930	F6A_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
931	F6A_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
932	F6A_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
933	F6A_HC_A89L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
934	F6A_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
935	F6A_HC_A89T - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
936	F6A_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
937	F6A_HC_A89V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
938	F6A_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
939	F6A_HC_L52M - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
940	F6A_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
941	F6A_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
942	F6A_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
943	F6A_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
944	F6A_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
945	F6A_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
946	F6A_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
947	F6A_HC_L52V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
948	F6A_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWRQAPGKGEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
949	F6A_HC_L52V	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP

	LC_V44F - VL		GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
950	F6A_HC_L52V LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
951	F6A_HC_L52V LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
952	F6A_HC_M41F A89V - HCDR1	artificial	IYAFN
953	F6A_HC_M41F A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
954	F6A_HC_M41F A89V - HCDR3	artificial	HGNFGNSYVSFFAY
955	F6A_HC_M41F A89V - LCDR1	artificial	GSSTGAVTSGYYPN
956	F6A_HC_M41F A89V - LCDR2	artificial	GTKFLAP
957	F6A_HC_M41F A89V - LCDR3	artificial	ALWYSNRWV
958	F6A_HC_M41F A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
959	F6A_HC_M41F A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
960	F6A_HC_M41I - HCDR1	artificial	IYAIN
961	F6A_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKS
962	F6A_HC_M41I - HCDR3	artificial	HGNFGNSYVSFFAY
963	F6A_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
964	F6A_HC_M41I - LCDR2	artificial	GTKFLAP
965	F6A_HC_M41I - LCDR3	artificial	ALWYSNRWV
966	F6A_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
967	F6A_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
968	F6A_HC_M41I A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
969	F6A_HC_M41I A89L - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
970	F6A_HC_M41I A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
971	F6A_HC_M41I A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
972	F6A_HC_M41I A89V_LC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
973	F6A_HC_M41I A89V_LC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
974	F6A_HC_M41I A89V_LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
975	F6A_HC_M41I A89V_LC_Q4 6K - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFSGGKTLTVL
976	F6A_HC_M41I L52V_A89V LC_L21I_Q46 K_G141S_V44	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGVWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS

	F - VH		
977	F6A_HC_M41I _L52V_A89V _LC_L21I_Q46 _K_G141S_V44 F - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
978	F6A_HC_M41I _LC_L21I_Q4 _6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
979	F6A_HC_M41I _LC_L21I_Q4 _6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
980	F6A_HC_M41I _Q46E_A89V _LC_L21I_Q46 _K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
981	F6A_HC_M41I _Q46E_A89V _LC_L21I_Q46 _K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
982	F6A_HC_M41V - HCDR1	artificial	IYAVN
983	F6A_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
984	F6A_HC_M41V - HCDR3	artificial	HGNFGNSYVSFFAY
985	F6A_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
986	F6A_HC_M41V - LCDR2	artificial	GTKFLAP
987	F6A_HC_M41V - LCDR3	artificial	ALWYSNRWV
988	F6A_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
989	F6A_HC_M41V - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
990	F6A_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
991	F6A_HC_Q46D - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
992	F6A_HC_Q46D _LC_L21I_Q4 _6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
993	F6A_HC_Q46D _LC_L21I_Q4 _6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
994	F6A_HC_Q46D _LC_L21I_Q4 _6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
995	F6A_HC_Q46D _LC_L21I_Q4 _6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
996	F6A_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
997	F6A_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
998	F6A_HC_Q46D _LC_Q46K_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
999	F6A_HC_Q46D _LC_Q46K_G1 _41S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWFQKKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1000	F6A_HC_Q46D _LC_Q46R -	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG

	VH		QGTlVTVSS
1001	F6A_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQRKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL
1002	F6A_HC_Q46D _LC_Q46R_G1 41s - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1003	F6A_HC_Q46D _LC_Q46R_G1 41s - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQRKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGSGtKLTlVL
1004	F6A_HC_Q46E - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1005	F6A_HC_Q46E - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL
1006	F6A_HC_Q46E _LC_L21I_Q4 6K_G141s - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1007	F6A_HC_Q46E _LC_L21I_Q4 6K_G141s - VL	artificial	QTVVTQEPsLTVSPGGTVTiTCGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGSGtKLTlVL
1008	F6A_HC_Q46E _LC_L21I_Q4 6R_G141s - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1009	F6A_HC_Q46E _LC_L21I_Q4 6R_G141s - VL	artificial	QTVVTQEPsLTVSPGGTVTiTCGSSTGAVTSgYYPNwVQRKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGSGtKLTlVL
1010	F6A_HC_Q46E _LC_Q46K - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1011	F6A_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL
1012	F6A_HC_Q46E _LC_Q46K_G1 41s - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1013	F6A_HC_Q46E _LC_Q46K_G1 41s - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGSGtKLTlVL
1014	F6A_HC_Q46E _LC_Q46R - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1015	F6A_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQRKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL
1016	F6A_HC_Q46E _LC_Q46R_G1 41s - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1017	F6A_HC_Q46E _LC_Q46R_G1 41s - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQRKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGSGtKLTlVL
1018	F6A_HC_Q46K - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVRKAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1019	F6A_HC_Q46K - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL
1020	F6A_HC_Q46R - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVRRAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCVRHGnFGNSYVSFFAYWG QGTlVTVSS
1021	F6A_HC_Q46R - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL
1022	F6A_HC_V107 A - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCARHGnFGNSYVSFFAYWG QGTlVTVSS
1023	F6A_HC_V107 A - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL
1024	F6A_HC_V107 L - VH	artificial	EVQlVESGGGLVQPGGSKLSCAASGFTFNiYAMNwVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSknTAYLQMNnLKTEDTAVYYCLRHGnFGNSYVSFFAYWG QGTlVTVSS
1025	F6A_HC_V107 L - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNwVQKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLsGVQPEDEAEYYCALWYSNRwVFGGGtKLTlVL

1026	F6A_I2E - HCDR1	artificial	IYAIN
1027	F6A_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1028	F6A_I2E - HCDR3	artificial	AGNFGSSYVSFFAY
1029	F6A_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1030	F6A_I2E - LCDR2	artificial	GTKFLAP
1031	F6A_I2E - LCDR3	artificial	ALWYSNRWV
1032	F6A_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKSRTTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYVSFFAYWG QGTLVTVSS
1033	F6A_I2E - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1034	F6A_I2K - HCDR1	artificial	IYAMN
1035	F6A_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1036	F6A_I2K - HCDR3	artificial	NENIGTSYVSFFAY
1037	F6A_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1038	F6A_I2K - LCDR2	artificial	GTKFLAP
1039	F6A_I2K - LCDR3	artificial	ALWYSNRWV
1040	F6A_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYVSFFAYWG QGTLVTVSS
1041	F6A_I2K - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1042	F6A_I2L - HCDR1	artificial	IYAMN
1043	F6A_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1044	F6A_I2L - HCDR3	artificial	AGNFGSSYVSFFAY
1045	F6A_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1046	F6A_I2L - LCDR2	artificial	GTKFLAP
1047	F6A_I2L - LCDR3	artificial	ALYYSNRWV
1048	F6A_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKSRTTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYVSFFAYWG QGTLVTVSS
1049	F6A_I2L - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1050	F6A_I2M - HCDR1	artificial	IYAMN
1051	F6A_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1052	F6A_I2M - HCDR3	artificial	AGNFGTSYVSFFAY
1053	F6A_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1054	F6A_I2M - LCDR2	artificial	GTKFLAP
1055	F6A_I2M - LCDR3	artificial	ALWYSNRWV
1056	F6A_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKSRTTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYVSFFAYWG QGTLVTVSS
1057	F6A_I2M - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1058	F6A_I2M2 - HCDR1	artificial	IYAIN
1059	F6A_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1060	F6A_I2M2 - HCDR3	artificial	NANFGTSYVSFFAY
1061	F6A_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN

1062	F6A_I2M2 - LCDR2	artificial	GTKFLAP
1063	F6A_I2M2 - LCDR3	artificial	ALWYSNRWV
1064	F6A_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYVSFFAYWG QGTLVTVSS
1065	F6A_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1066	F6A_LC_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1067	F6A_LC_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1068	F6A_LC_G141S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1069	F6A_LC_G141S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1070	F6A_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1071	F6A_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1072	F6A_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1073	F6A_LC_L83S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1074	F6A_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1075	F6A_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1076	F6A_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1077	F6A_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1078	F6A_LC_A107L - HCDR1	artificial	IYAMN
1079	F6A_LC_A107L - HCDR2	artificial	RIRSKYNNYATYYADSVKS
1080	F6A_LC_A107L - HCDR3	artificial	HGNFGNSYVSFFAY
1081	F6A_LC_A107L - LCDR1	artificial	GSSTGAVTSGYYPN
1082	F6A_LC_A107L - LCDR2	artificial	GTKFLAP
1083	F6A_LC_A107L - LCDR3	artificial	LLWYSNRWV
1084	F6A_LC_A107L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1085	F6A_LC_A107L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLWYSNRWVFGSGTKLTVL
1086	F6A_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1087	F6A_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1088	F6A_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1089	F6A_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1090	F6A_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1091	F6A_LC_V44M - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1092	F6A_LC_W109Y - HCDR1	artificial	IYAMN
1093	F6A_LC_W109Y - HCDR2	artificial	RIRSKYNNYATYYADSVKS

1094	F6A_LC_W109 Y - HCDR3	artificial	HGNFGNSYVSFFAY
1095	F6A_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1096	F6A_LC_W109 Y - LCDR2	artificial	GTKFLAP
1097	F6A_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1098	F6A_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1099	F6A_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1100	F7O - HCDR1	artificial	VYAMN
1101	F7O - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1102	F7O - HCDR3	artificial	HGNFGNSYISWWAY
1103	F7O - LCDR1	artificial	GSSTGAVTSGYYPN
1104	F7O - LCDR2	artificial	GTKFLAP
1105	F7O - LCDR3	artificial	ALWYSNRWV
1106	F7O - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1107	F7O - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1108	F7O_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLMNNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1109	F7O_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1110	F7O_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1111	F7O_HC_A89L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1112	F7O_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1113	F7O_HC_A89T - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1114	F7O_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1115	F7O_HC_A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1116	F7O_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1117	F7O_HC_L52M - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1118	F7O_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1119	F7O_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1120	F7O_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1121	F7O_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1122	F7O_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1123	F7O_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1124	F7O_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIVAMNWRQAPGKGEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS

1125	F70_HC_L52V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1126	F70_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGVFWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1127	F70_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1128	F70_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGVFWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1129	F70_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1130	F70_HC_M41F _A89V - HCDR1	artificial	VYAFN
1131	F70_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1132	F70_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYISWWAY
1133	F70_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1134	F70_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1135	F70_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1136	F70_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1137	F70_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1138	F70_HC_M41I - HCDR1	artificial	VYAIN
1139	F70_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1140	F70_HC_M41I - HCDR3	artificial	HGNFGNSYISWWAY
1141	F70_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
1142	F70_HC_M41I - LCDR2	artificial	GTKFLAP
1143	F70_HC_M41I - LCDR3	artificial	ALWYSNRWV
1144	F70_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1145	F70_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1146	F70_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1147	F70_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1148	F70_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1149	F70_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1150	F70_HC_M41I _A89V_LC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1151	F70_HC_M41I _A89V_LC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1152	F70_HC_M41I _A89V_LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS

1153	F70_HC_M41I _A89V_LC_Q4 6K - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1154	F70_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1155	F70_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1156	F70_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1157	F70_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1158	F70_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1159	F70_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1160	F70_HC_M41V - HCDRI	artificial	VYAVN
1161	F70_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1162	F70_HC_M41V - HCDR3	artificial	HGNFGNSYISWWAY
1163	F70_HC_M41V - LCDRI	artificial	GSSTGAVTSGYYPN
1164	F70_HC_M41V - LCDR2	artificial	GTKFLAP
1165	F70_HC_M41V - LCDR3	artificial	ALWYSNRWV
1166	F70_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1167	F70_HC_M41V - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1168	F70_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1169	F70_HC_Q46D - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1170	F70_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1171	F70_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1172	F70_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1173	F70_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1174	F70_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1175	F70_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1176	F70_HC_Q46D	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY

	LC_Q46K_G1 41S - VH		ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1177	F70_HC_Q46D LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1178	F70_HC_Q46D LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1179	F70_HC_Q46D LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1180	F70_HC_Q46D LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1181	F70_HC_Q46D LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1182	F70_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1183	F70_HC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1184	F70_HC_Q46E LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1185	F70_HC_Q46E LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1186	F70_HC_Q46E LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1187	F70_HC_Q46E LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1188	F70_HC_Q46E LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1189	F70_HC_Q46E LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1190	F70_HC_Q46E LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1191	F70_HC_Q46E LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1192	F70_HC_Q46E LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1193	F70_HC_Q46E LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1194	F70_HC_Q46E LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1195	F70_HC_Q46E LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1196	F70_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1197	F70_HC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1198	F70_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1199	F70_HC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1200	F70_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYISWWAYWG QGTLVTVSS
1201	F70_HC_V107	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP

	A - VL		GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1202	F70_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYISWWAYWG QGTLVTVSS
1203	F70_HC_V107 L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1204	F70_HC_W136 F - HCDR1	artificial	VYAMN
1205	F70_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1206	F70_HC_W136 F - HCDR3	artificial	HGNFGNSYISWFAY
1207	F70_HC_W136 F - LCDR1	artificial	GSSTGAVTSGYYPN
1208	F70_HC_W136 F - LCDR2	artificial	GTKFLAP
1209	F70_HC_W136 F - LCDR3	artificial	ALWYSNRWV
1210	F70_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWFAYWG QGTLVTVSS
1211	F70_HC_W136 F - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1212	F70_HC_W136 F LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWFAYWG QGTLVTVSS
1213	F70_HC_W136 F LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1214	F70_HC_W136 F LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWFAYWG QGTLVTVSS
1215	F70_HC_W136 F LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1216	F70_I2E - HCDR1	artificial	VYAIN
1217	F70_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1218	F70_I2E - HCDR3	artificial	AGNFGSSYISWWAY
1219	F70_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1220	F70_I2E - LCDR2	artificial	GTKFLAP
1221	F70_I2E - LCDR3	artificial	ALWYSNRWV
1222	F70_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAINWRQAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISWWAYWG QGTLVTVSS
1223	F70_I2E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1224	F70_I2K - HCDR1	artificial	VYAMN
1225	F70_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1226	F70_I2K - HCDR3	artificial	NENIGTSYISWWAY
1227	F70_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1228	F70_I2K - LCDR2	artificial	GTKFLAP
1229	F70_I2K - LCDR3	artificial	ALWYSNRWV
1230	F70_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNVYAMNWRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISWWAYWG QGTLVTVSS
1231	F70_I2K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1232	F70_I2L - HCDR1	artificial	VYAMN
1233	F70_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1234	F70_I2L - HCDR3	artificial	AGNFGSSYISWFAY

1235	F70_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1236	F70_I2L - LCDR2	artificial	GTKFLAP
1237	F70_I2L - LCDR3	artificial	ALYYSNRWV
1238	F70_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISWFAYWG QGTLVTVSS
1239	F70_I2L - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1240	F70_I2M - HCDR1	artificial	VYAMN
1241	F70_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1242	F70_I2M - HCDR3	artificial	AGNFGTSYISWWAY
1243	F70_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1244	F70_I2M - LCDR2	artificial	GTKFLAP
1245	F70_I2M - LCDR3	artificial	ALWYSNRWV
1246	F70_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISWWAYWG QGTLVTVSS
1247	F70_I2M - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1248	F70_I2M2 - HCDR1	artificial	VYAIN
1249	F70_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1250	F70_I2M2 - HCDR3	artificial	NANFGTSYISWFAY
1251	F70_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1252	F70_I2M2 - LCDR2	artificial	GTKFLAP
1253	F70_I2M2 - LCDR3	artificial	ALWYSNRWV
1254	F70_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISWFAYWG QGTLVTVSS
1255	F70_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1256	F70_LC_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1257	F70_LC_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1258	F70_LC_G141S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1259	F70_LC_G141S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1260	F70_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1261	F70_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1262	F70_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1263	F70_LC_L83S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1264	F70_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1265	F70_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1266	F70_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1267	F70_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

1268	F70_LC_A107 L - HCDR1	artificial	VYAMN
1269	F70_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1270	F70_LC_A107 L - HCDR3	artificial	HGNFGNSYISWWAY
1271	F70_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1272	F70_LC_A107 L - LCDR2	artificial	GTKFLAP
1273	F70_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1274	F70_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1275	F70_LC_A107 L - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1276	F70_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1277	F70_LC_V44I - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1278	F70_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1279	F70_LC_V44L - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1280	F70_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1281	F70_LC_V44M - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1282	F70_LC_W109 Y - HCDR1	artificial	VYAMN
1283	F70_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1284	F70_LC_W109 Y - HCDR3	artificial	HGNFGNSYISWWAY
1285	F70_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1286	F70_LC_W109 Y - LCDR2	artificial	GTKFLAP
1287	F70_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1288	F70_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1289	F70_LC_W109 Y - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
1290	G4H - HCDR1	artificial	RYAMN
1291	G4H - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1292	G4H - HCDR3	artificial	HGNFGNSYLSYFAY
1293	G4H - LCDR1	artificial	GSSTGAVTSGYYPN
1294	G4H - LCDR2	artificial	GTKFLAP
1295	G4H - LCDR3	artificial	ALWYSNRWV
1296	G4H - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1297	G4H - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1298	G4H_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1299	G4H_HC_A89I - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1300	G4H_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1301	G4H_HC_A89L - VL	artificial	QTVVTQEPSLTVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1302	G4H_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG

			QGTILVTVSS
1303	G4H_HC_A89T - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1304	G4H_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1305	G4H_HC_A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1306	G4H_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1307	G4H_HC_L52M - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1308	G4H_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1309	G4H_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1310	G4H_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1311	G4H_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1312	G4H_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1313	G4H_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1314	G4H_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGVEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1315	G4H_HC_L52V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1316	G4H_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGVEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1317	G4H_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1318	G4H_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGVEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1319	G4H_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1320	G4H_HC_M41F _A89V - HCDR1	artificial	RYAFN
1321	G4H_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1322	G4H_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYLSYFAY
1323	G4H_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1324	G4H_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1325	G4H_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1326	G4H_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTILVTVSS
1327	G4H_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1328	G4H_HC_M41I - HCDR1	artificial	RYAFN

1329	G4H_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1330	G4H_HC_M41I - HCDR3	artificial	HGNFGNSYLSYFAY
1331	G4H_HC_M41I - LCDRI	artificial	GSSTGAVTSGYYPN
1332	G4H_HC_M41I - LCDR2	artificial	GTKFLAP
1333	G4H_HC_M41I - LCDR3	artificial	ALWYSNRWV
1334	G4H_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1335	G4H_HC_M41I - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGLTKLTVL
1336	G4H_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1337	G4H_HC_M41I _A89L - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGLTKLTVL
1338	G4H_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1339	G4H_HC_M41I _A89V - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGLTKLTVL
1340	G4H_HC_M41I _A89V LC L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1341	G4H_HC_M41I _A89V LC L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1342	G4H_HC_M41I _A89V LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1343	G4H_HC_M41I _A89V LC_Q4 6K - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGLTKLTVL
1344	G4H_HC_M41I _L52V A89V LC L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1345	G4H_HC_M41I _L52V A89V LC L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1346	G4H_HC_M41I _LC L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1347	G4H_HC_M41I _LC L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1348	G4H_HC_M41I _Q46E A89V LC L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1349	G4H_HC_M41I _Q46E A89V LC L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1350	G4H_HC_M41V - HCDR1	artificial	RYAVN
1351	G4H_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1352	G4H_HC_M41V - HCDR3	artificial	HGNFGNSYLSYFAY
1353	G4H_HC_M41V - LCDRI	artificial	GSSTGAVTSGYYPN
1354	G4H_HC_M41V	artificial	GTKFLAP

	- LCDR2		
1355	G4H_HC_M41V - LCDR3	artificial	ALWYSNRWV
1356	G4H_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1357	G4H_HC_M41V - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1358	G4H_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1359	G4H_HC_Q46D - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1360	G4H_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1361	G4H_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1362	G4H_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1363	G4H_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1364	G4H_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1365	G4H_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1366	G4H_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1367	G4H_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1368	G4H_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1369	G4H_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1370	G4H_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1371	G4H_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1372	G4H_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1373	G4H_HC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1374	G4H_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1375	G4H_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1376	G4H_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1377	G4H_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1378	G4H_HC_Q46E _LC_Q46K -	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG

	VH		QGTLVTVSS
1379	G4H_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1380	G4H_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1381	G4H_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1382	G4H_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1383	G4H_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1384	G4H_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1385	G4H_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1386	G4H_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1387	G4H_HC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1388	G4H_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1389	G4H_HC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1390	G4H_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYLSYFAYWG QGTLVTVSS
1391	G4H_HC_V107 A - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1392	G4H_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYLSYFAYWG QGTLVTVSS
1393	G4H_HC_V107 L - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1394	G4H_I2E - HCDR1	artificial	RYAIN
1395	G4H_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1396	G4H_I2E - HCDR3	artificial	AGNFGSSYLSYFAY
1397	G4H_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1398	G4H_I2E - LCDR2	artificial	GTKFLAP
1399	G4H_I2E - LCDR3	artificial	ALWYSNRWV
1400	G4H_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYLSYFAYWG QGTLVTVSS
1401	G4H_I2E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1402	G4H_I2K - HCDR1	artificial	RYAMN
1403	G4H_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1404	G4H_I2K - HCDR3	artificial	NENIGTSYLSYFAY
1405	G4H_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1406	G4H_I2K - LCDR2	artificial	GTKFLAP
1407	G4H_I2K - LCDR3	artificial	ALWYSNRWV
1408	G4H_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYLSYFAYWG QGTLVTVSS
1409	G4H_I2K -	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP

	VL		GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1410	G4H_I2L - HCDR1	artificial	RYAMN
1411	G4H_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1412	G4H_I2L - HCDR3	artificial	AGNFGSSYLSYFAY
1413	G4H_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1414	G4H_I2L - LCDR2	artificial	GTKFLAP
1415	G4H_I2L - LCDR3	artificial	ALYYSNRWV
1416	G4H_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYLSYFAYWG QGTLVTVSS
1417	G4H_I2L - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1418	G4H_I2M - HCDR1	artificial	RYAMN
1419	G4H_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1420	G4H_I2M - HCDR3	artificial	AGNFGTSYLSYFAY
1421	G4H_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1422	G4H_I2M - LCDR2	artificial	GTKFLAP
1423	G4H_I2M - LCDR3	artificial	ALWYSNRWV
1424	G4H_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYLSYFAYWG QGTLVTVSS
1425	G4H_I2M - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1426	G4H_I2M2 - HCDR1	artificial	RYAIN
1427	G4H_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1428	G4H_I2M2 - HCDR3	artificial	NANFGTSYLSYFAY
1429	G4H_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1430	G4H_I2M2 - LCDR2	artificial	GTKFLAP
1431	G4H_I2M2 - LCDR3	artificial	ALWYSNRWV
1432	G4H_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVREAPGKLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYLSYFAYWG QGTLVTVSS
1433	G4H_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1434	G4H_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1435	G4H_LC_G141 S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1436	G4H_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1437	G4H_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1438	G4H_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1439	G4H_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1440	G4H_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1441	G4H_LC_L83S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1442	G4H_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS

1443	G4H_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1444	G4H_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1445	G4H_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1446	G4H_LC_A107 L - HCDR1	artificial	RYAMN
1447	G4H_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKGG
1448	G4H_LC_A107 L - HCDR3	artificial	HGNFGNSYLSYFAY
1449	G4H_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1450	G4H_LC_A107 L - LCDR2	artificial	GTKFLAP
1451	G4H_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1452	G4H_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1453	G4H_LC_A107 L - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1454	G4H_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1455	G4H_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1456	G4H_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1457	G4H_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1458	G4H_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1459	G4H_LC_V44M - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1460	G4H_LC_W109 Y - HCDR1	artificial	RYAMN
1461	G4H_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKGG
1462	G4H_LC_W109 Y - HCDR3	artificial	HGNFGNSYLSYFAY
1463	G4H_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1464	G4H_LC_W109 Y - LCDR2	artificial	GTKFLAP
1465	G4H_LC_W109 Y - LCDR3	artificial	ALWYSNRWV
1466	G4H_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1467	G4H_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1468	H1E - HCDR1	artificial	SYAMN
1469	H1E - HCDR2	artificial	RIRSKYNNYATYYADSVKGG
1470	H1E - HCDR3	artificial	HGNFGNSYLSFWAY
1471	H1E - LCDR1	artificial	GSSTGAVTSGYYPN
1472	H1E - LCDR2	artificial	GTKFLAP
1473	H1E - LCDR3	artificial	ALWYSNRWV
1474	H1E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1475	H1E - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL
1476	H1E_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1477	H1E_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFVGGGTKLTVL

1478	H1E_HC_A89L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1479	H1E_HC_A89L - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1480	H1E_HC_A89T - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1481	H1E_HC_A89T - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1482	H1E_HC_A89V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1483	H1E_HC_A89V - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1484	H1E_HC_L52M - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1485	H1E_HC_L52M - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1486	H1E_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1487	H1E_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1488	H1E_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1489	H1E_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1490	H1E_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1491	H1E_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1492	H1E_HC_L52V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1493	H1E_HC_L52V - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1494	H1E_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1495	H1E_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1496	H1E_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1497	H1E_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1498	H1E_HC_M41F _A89V - HCDR1	artificial	SYAFN
1499	H1E_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1500	H1E_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYLSFWAY
1501	H1E_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1502	H1E_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1503	H1E_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1504	H1E_HC_M41F	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAFNWVRQAPGKGLEWVARIRSKYNNY

	_A89V - VH		ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1505	H1E_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1506	H1E_HC_M41I - HCDR1	artificial	SYAIN
1507	H1E_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1508	H1E_HC_M41I - HCDR3	artificial	HGNFGNSYLSFWAY
1509	H1E_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
1510	H1E_HC_M41I - LCDR2	artificial	GTKFLAP
1511	H1E_HC_M41I - LCDR3	artificial	ALWYSNRWV
1512	H1E_HC_M41I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1513	H1E_HC_M41I - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1514	H1E_HC_M41I _A89L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1515	H1E_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1516	H1E_HC_M41I _A89V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1517	H1E_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1518	H1E_HC_M41I _A89V_LC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1519	H1E_HC_M41I _A89V_LC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1520	H1E_HC_M41I _A89V_LC_Q4 6K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1521	H1E_HC_M41I _A89V_LC_Q4 6K - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1522	H1E_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1523	H1E_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1524	H1E_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1525	H1E_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1526	H1E_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1527	H1E_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1528	H1E_HC_M41V - HCDR1	artificial	SYAVN
1529	H1E_HC_M41V	artificial	RIRSKYNNYATYYADSVKG

	- HCDR2		
1530	H1E_HC_M41V - HCDR3	artificial	HGNFGNSYLSFWAY
1531	H1E_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
1532	H1E_HC_M41V - LCDR2	artificial	GTKFLAP
1533	H1E_HC_M41V - LCDR3	artificial	ALWYSNRWV
1534	H1E_HC_M41V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1535	H1E_HC_M41V - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
1536	H1E_HC_Q46D - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1537	H1E_HC_Q46D - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
1538	H1E_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1539	H1E_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1540	H1E_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1541	H1E_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1542	H1E_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1543	H1E_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
1544	H1E_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1545	H1E_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1546	H1E_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1547	H1E_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
1548	H1E_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1549	H1E_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1550	H1E_HC_Q46E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1551	H1E_HC_Q46E - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
1552	H1E_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1553	H1E_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1554	H1E_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS

1555	H1E_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1556	H1E_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1557	H1E_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1558	H1E_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1559	H1E_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1560	H1E_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1561	H1E_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1562	H1E_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1563	H1E_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1564	H1E_HC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1565	H1E_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1566	H1E_HC_Q46R - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1567	H1E_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1568	H1E_HC_V107 A - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYLSFWAYWG QGTLVTVSS
1569	H1E_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1570	H1E_HC_V107 L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYLSFWAYWG QGTLVTVSS
1571	H1E_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1572	H1E_HC_W136 F - HCDR1	artificial	SYAMN
1573	H1E_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1574	H1E_HC_W136 F - HCDR3	artificial	HGNFGNSYLSFFAY
1575	H1E_HC_W136 F - LCDR1	artificial	GSSTGAVTSGYYPN
1576	H1E_HC_W136 F - LCDR2	artificial	GTKFLAP
1577	H1E_HC_W136 F - LCDR3	artificial	ALWYSNRWV
1578	H1E_HC_W136 F - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFFAYWG QGTLVTVSS
1579	H1E_HC_W136 F - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1580	H1E_HC_W136 F LC_V44I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFFAYWG QGTLVTVSS
1581	H1E_HC_W136 F LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1582	H1E_HC_W136 F LC_V44L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWNVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFFAYWG QGTLVTVSS
1583	H1E_HC_W136 F LC_V44L -	artificial	QTVVTQEPSTLTVSPGGTITITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

	VL		
1584	H1E_I2E - HCDR1	artificial	SYAIN
1585	H1E_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1586	H1E_I2E - HCDR3	artificial	AGNFGSSYLSFWAY
1587	H1E_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1588	H1E_I2E - LCDR2	artificial	GTKFLAP
1589	H1E_I2E - LCDR3	artificial	ALWYSNRWV
1590	H1E_I2E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYLSFWAYWG QGTLVTVSS
1591	H1E_I2E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1592	H1E_I2K - HCDR1	artificial	SYAMN
1593	H1E_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1594	H1E_I2K - HCDR3	artificial	NENIGTSYLSFWAY
1595	H1E_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1596	H1E_I2K - LCDR2	artificial	GTKFLAP
1597	H1E_I2K - LCDR3	artificial	ALWYSNRWV
1598	H1E_I2K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYLSFWAYWG QGTLVTVSS
1599	H1E_I2K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1600	H1E_I2L - HCDR1	artificial	SYAMN
1601	H1E_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1602	H1E_I2L - HCDR3	artificial	AGNFGSSYLSFFAY
1603	H1E_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1604	H1E_I2L - LCDR2	artificial	GTKFLAP
1605	H1E_I2L - LCDR3	artificial	ALYYSNRWV
1606	H1E_I2L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYLSFFAYWG QGTLVTVSS
1607	H1E_I2L - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWIQKPGQAPRGLIGGTFKFLAP GTPARFSGSLEGGKAALTLGSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1608	H1E_I2M - HCDR1	artificial	SYAMN
1609	H1E_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1610	H1E_I2M - HCDR3	artificial	AGNFGTSYLSFWAY
1611	H1E_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1612	H1E_I2M - LCDR2	artificial	GTKFLAP
1613	H1E_I2M - LCDR3	artificial	ALWYSNRWV
1614	H1E_I2M - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYLSFWAYWG QGTLVTVSS
1615	H1E_I2M - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1616	H1E_I2M2 - HCDR1	artificial	SYAIN
1617	H1E_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1618	H1E_I2M2 - HCDR3	artificial	NANFGTSYLSFFAY

1619	H1E_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1620	H1E_I2M2 - LCDR2	artificial	GTKFLAP
1621	H1E_I2M2 - LCDR3	artificial	ALWYSNRWV
1622	H1E_I2M2 - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYLSFFAYWG QGTLVTVSS
1623	H1E_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1624	H1E_LC_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1625	H1E_LC_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1626	H1E_LC_G141S_L21I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1627	H1E_LC_G141S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1628	H1E_LC_L83E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1629	H1E_LC_L83E - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1630	H1E_LC_L83S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1631	H1E_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1632	H1E_LC_Q46E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1633	H1E_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1634	H1E_LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1635	H1E_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1636	H1E_LC_A107L - HCDR1	artificial	SYAMN
1637	H1E_LC_A107L - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1638	H1E_LC_A107L - HCDR3	artificial	HGNFGNSYLSFWAY
1639	H1E_LC_A107L - LCDR1	artificial	GSSTGAVTSGYYPN
1640	H1E_LC_A107L - LCDR2	artificial	GTKFLAP
1641	H1E_LC_A107L - LCDR3	artificial	LLWYSNRWV
1642	H1E_LC_A107L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1643	H1E_LC_A107L - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWWQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLWYSNRWVFGSGTKLTVL
1644	H1E_LC_V44I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1645	H1E_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1646	H1E_LC_V44L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1647	H1E_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWLQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1648	H1E_LC_V44M - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1649	H1E_LC_V44M - VL	artificial	QTVVTQEPSTLTVSPGGTTLTCSSTGAVTSGYYPNWMQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1650	H1E_LC_W109Y - HCDR1	artificial	SYAMN

1651	H1E_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1652	H1E_LC_W109 Y - HCDR3	artificial	HGNFGNSYLSFWAY
1653	H1E_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1654	H1E_LC_W109 Y - LCDR2	artificial	GTKFLAP
1655	H1E_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1656	H1E_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1657	H1E_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
1658	H2C - HCDR1	artificial	KYAMN
1659	H2C - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1660	H2C - HCDR3	artificial	HGNFGNSYISYWAY
1661	H2C - LCDR1	artificial	GSSTGAVTSGYYPN
1662	H2C - LCDR2	artificial	GTKFLAP
1663	H2C - LCDR3	artificial	ALWYSNRWV
1664	H2C - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1665	H2C - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1666	H2C_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1667	H2C_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1668	H2C_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1669	H2C_HC_A89L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1670	H2C_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1671	H2C_HC_A89T - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1672	H2C_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1673	H2C_HC_A89V - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1674	H2C_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1675	H2C_HC_L52M - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1676	H2C_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1677	H2C_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1678	H2C_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1679	H2C_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1680	H2C_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1681	H2C_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1682	H2C_HC_L52V	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGEWVARIRSKYNNY

	- VH		ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1683	H2C_HC_L52V - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1684	H2C_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1685	H2C_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1686	H2C_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1687	H2C_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1688	H2C_HC_M41F _A89V - HCDR1	artificial	KYAFN
1689	H2C_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1690	H2C_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYISYWAY
1691	H2C_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1692	H2C_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1693	H2C_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1694	H2C_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1695	H2C_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1696	H2C_HC_M41I - HCDR1	artificial	KYAIN
1697	H2C_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1698	H2C_HC_M41I - HCDR3	artificial	HGNFGNSYISYWAY
1699	H2C_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
1700	H2C_HC_M41I - LCDR2	artificial	GTKFLAP
1701	H2C_HC_M41I - LCDR3	artificial	ALWYSNRWV
1702	H2C_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1703	H2C_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1704	H2C_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1705	H2C_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1706	H2C_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1707	H2C_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1708	H2C_HC_M41I _A89V LC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1709	H2C_HC_M41I _A89V LC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1710	H2C_HC_M41I _A89V LC_Q4	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG

	6K - VH		QGTlVTVSS
1711	H2C_HC_M41I _A89V_LC_Q4 6K - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1712	H2C_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1713	H2C_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPsLTVSPGGTVTITcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1714	H2C_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1715	H2C_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPsLTVSPGGTVTITcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1716	H2C_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1717	H2C_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPsLTVSPGGTVTITcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1718	H2C_HC_M41V - HCDR1	artificial	KYAVN
1719	H2C_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1720	H2C_HC_M41V - HCDR3	artificial	HGNFGNSYISYWAY
1721	H2C_HC_M41V - LCDR1	artificial	GSSTGAVTSgYYPN
1722	H2C_HC_M41V - LCDR2	artificial	GtKFLAP
1723	H2C_HC_M41V - LCDR3	artificial	ALWYSNRWV
1724	H2C_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAVNWVRQAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1725	H2C_HC_M41V - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1726	H2C_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1727	H2C_HC_Q46D - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1728	H2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1729	H2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPsLTVSPGGTVTITcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1730	H2C_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1731	H2C_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPsLTVSPGGTVTITcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL
1732	H2C_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNnLKTEDTAVYYCVRHGnFGNSYISYWAYWG QGTlVTVSS
1733	H2C_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPsLTVSPGGTVTLTcGSSTGAVTSgYYPNWVQKKPGQAPRGLIGGtKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGtKLTVL

1734	H2C_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1735	H2C_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1736	H2C_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1737	H2C_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1738	H2C_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1739	H2C_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1740	H2C_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1741	H2C_HC_Q46E - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1742	H2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1743	H2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1744	H2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1745	H2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1746	H2C_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1747	H2C_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1748	H2C_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1749	H2C_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1750	H2C_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1751	H2C_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1752	H2C_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1753	H2C_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1754	H2C_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1755	H2C_HC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1756	H2C_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1757	H2C_HC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1758	H2C_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYISYWAYWG QGTLVTVSS

1759	H2C_HC_V107 A - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1760	H2C_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYISYWAYWG QGTLVTVSS
1761	H2C_HC_V107 L - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1762	H2C_HC_W136 F - HCDR1	artificial	KYAMN
1763	H2C_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1764	H2C_HC_W136 F - HCDR3	artificial	HGNFGNSYISYFAY
1765	H2C_HC_W136 F - LCDR1	artificial	GSSTGAVTSGYYPN
1766	H2C_HC_W136 F - LCDR2	artificial	GTKFLAP
1767	H2C_HC_W136 F - LCDR3	artificial	ALWYSNRWV
1768	H2C_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1769	H2C_HC_W136 F - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1770	H2C_HC_W136 F_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1771	H2C_HC_W136 F_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWIQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1772	H2C_HC_W136 F_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1773	H2C_HC_W136 F_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWLQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1774	H2C_I2E - HCDR1	artificial	KYAIN
1775	H2C_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1776	H2C_I2E - HCDR3	artificial	AGNFGSSYISYWAY
1777	H2C_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1778	H2C_I2E - LCDR2	artificial	GTKFLAP
1779	H2C_I2E - LCDR3	artificial	ALWYSNRWV
1780	H2C_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCARAGNFGSSYISYWAYWG QGTLVTVSS
1781	H2C_I2E - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1782	H2C_I2K - HCDR1	artificial	KYAMN
1783	H2C_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1784	H2C_I2K - HCDR3	artificial	NENIGTSYISYWAY
1785	H2C_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1786	H2C_I2K - LCDR2	artificial	GTKFLAP
1787	H2C_I2K - LCDR3	artificial	ALWYSNRWV
1788	H2C_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRNENIGTSYISYWAYWG QGTLVTVSS
1789	H2C_I2K - VL	artificial	QTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1790	H2C_I2L - HCDR1	artificial	KYAMN
1791	H2C_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1792	H2C_I2L - HCDR3	artificial	AGNFGSSYISYFAY

1793	H2C_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1794	H2C_I2L - LCDR2	artificial	GTKFLAP
1795	H2C_I2L - LCDR3	artificial	ALYYSNRWV
1796	H2C_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWG QGTLVTVSS
1797	H2C_I2L - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1798	H2C_I2M - HCDR1	artificial	KYAMN
1799	H2C_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1800	H2C_I2M - HCDR3	artificial	AGNFGTSYISYWAY
1801	H2C_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1802	H2C_I2M - LCDR2	artificial	GTKFLAP
1803	H2C_I2M - LCDR3	artificial	ALWYSNRWV
1804	H2C_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWG QGTLVTVSS
1805	H2C_I2M - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1806	H2C_I2M2 - HCDR1	artificial	KYAIN
1807	H2C_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1808	H2C_I2M2 - HCDR3	artificial	NANFGTSYISYFAY
1809	H2C_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1810	H2C_I2M2 - LCDR2	artificial	GTKFLAP
1811	H2C_I2M2 - LCDR3	artificial	ALWYSNRWV
1812	H2C_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWG QGTLVTVSS
1813	H2C_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1814	H2C_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1815	H2C_LC_G141 S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1816	H2C_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1817	H2C_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1818	H2C_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1819	H2C_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1820	H2C_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1821	H2C_LC_L83S - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1822	H2C_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1823	H2C_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1824	H2C_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1825	H2C_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTITITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

1826	H2C_LC_A107 L - HCDR1	artificial	KYAMN
1827	H2C_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1828	H2C_LC_A107 L - HCDR3	artificial	HGNFGNSYISYWAY
1829	H2C_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1830	H2C_LC_A107 L - LCDR2	artificial	GTKFLAP
1831	H2C_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1832	H2C_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1833	H2C_LC_A107 L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCCLWYSNRWVFGGGTKLTVL
1834	H2C_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1835	H2C_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWIQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1836	H2C_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1837	H2C_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWLQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1838	H2C_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1839	H2C_LC_V44M - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWMQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1840	H2C_LC_W109 Y - HCDR1	artificial	KYAMN
1841	H2C_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1842	H2C_LC_W109 Y - HCDR3	artificial	HGNFGNSYISYWAY
1843	H2C_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1844	H2C_LC_W109 Y - LCDR2	artificial	GTKFLAP
1845	H2C_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1846	H2C_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1847	H2C_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
1848	I2C - HCDR1	artificial	KYAMN
1849	I2C - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1850	I2C - HCDR3	artificial	HGNFGNSYISYWAY
1851	I2C - LCDR1	artificial	GSSTGAVTSGNYPN
1852	I2C - LCDR2	artificial	GTKFLAP
1853	I2C - LCDR3	artificial	VLWYSNRWV
1854	I2C - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1855	I2C - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1856	I2C_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1857	I2C_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1858	I2C_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1859	I2C_HC_A89L - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1860	I2C_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG

			QGTLVTVSS
1861	I2C_HC_A89T - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1862	I2C_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1863	I2C_HC_A89V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1864	I2C_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1865	I2C_HC_L52M - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1866	I2C_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1867	I2C_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1868	I2C_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1869	I2C_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1870	I2C_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1871	I2C_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1872	I2C_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1873	I2C_HC_L52V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1874	I2C_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1875	I2C_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1876	I2C_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1877	I2C_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1878	I2C_HC_M41F _A89V - HCDR1	artificial	KYAFN
1879	I2C_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1880	I2C_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYISYWAY
1881	I2C_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGNYPN
1882	I2C_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1883	I2C_HC_M41F _A89V - LCDR3	artificial	VLWYSNRWV
1884	I2C_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1885	I2C_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1886	I2C_HC_M41I - HCDR1	artificial	KYAIN

1887	I2C_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1888	I2C_HC_M41I - HCDR3	artificial	HGNFGNSYISYWAY
1889	I2C_HC_M41I - LCDRI	artificial	GSSTGAVTSGNYPN
1890	I2C_HC_M41I - LCDR2	artificial	GTKFLAP
1891	I2C_HC_M41I - LCDR3	artificial	VLWYSNRWV
1892	I2C_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1893	I2C_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1894	I2C_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1895	I2C_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1896	I2C_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1897	I2C_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1898	I2C_HC_M41I _A89V LC L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1899	I2C_HC_M41I _A89V LC L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1900	I2C_HC_M41I _A89V LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1901	I2C_HC_M41I _A89V LC_Q4 6K - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1902	I2C_HC_M41I _L52V A89V LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1903	I2C_HC_M41I _L52V A89V LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1904	I2C_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1905	I2C_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1906	I2C_HC_M41I _Q46E A89V LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1907	I2C_HC_M41I _Q46E A89V LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTITLCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1908	I2C_HC_M41V - HCDR1	artificial	KYAVN
1909	I2C_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1910	I2C_HC_M41V - HCDR3	artificial	HGNFGNSYISYWAY
1911	I2C_HC_M41V - LCDRI	artificial	GSSTGAVTSGNYPN
1912	I2C_HC_M41V	artificial	GTKFLAP

	- LCDR2		
1913	I2C_HC_M41V - LCDR3	artificial	VLWYSNRWV
1914	I2C_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1915	I2C_HC_M41V - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1916	I2C_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1917	I2C_HC_Q46D - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1918	I2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1919	I2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1920	I2C_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1921	I2C_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1922	I2C_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1923	I2C_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1924	I2C_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1925	I2C_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1926	I2C_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1927	I2C_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1928	I2C_HC_Q46D _LC_L21I_Q 46R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1929	I2C_HC_Q46D _LC_L21I_Q 46R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1930	I2C_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1931	I2C_HC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1932	I2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1933	I2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1934	I2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1935	I2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1936	I2C_HC_Q46E _LC_Q46K -	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG

	VH		QGTLVTVSS
1937	I2C_HC_Q46E _LC_Q46K - _VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1938	I2C_HC_Q46E _LC_Q46K_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1939	I2C_HC_Q46E _LC_Q46K_G1 _41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1940	I2C_HC_Q46E _LC_Q46R - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1941	I2C_HC_Q46E _LC_Q46R - _VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1942	I2C_HC_Q46E _LC_Q46R_G1 _41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1943	I2C_HC_Q46E _LC_Q46R_G1 _41S - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1944	I2C_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1945	I2C_HC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1946	I2C_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1947	I2C_HC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1948	I2C_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYISYWAYWG QGTLVTVSS
1949	I2C_HC_V107 A - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1950	I2C_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYISYWAYWG QGTLVTVSS
1951	I2C_HC_V107 L - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1952	I2C_HC_W136 F - HCDR1	artificial	KYAMN
1953	I2C_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1954	I2C_HC_W136 F - HCDR3	artificial	HGNFGNSYISYFAY
1955	I2C_HC_W136 F - LCDR1	artificial	GSSTGAVTSGNYPN
1956	I2C_HC_W136 F - LCDR2	artificial	GTKFLAP
1957	I2C_HC_W136 F - LCDR3	artificial	VLWYSNRWV
1958	I2C_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1959	I2C_HC_W136 F - VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1960	I2C_HC_W136 F_LC_V44I - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1961	I2C_HC_W136 F_LC_V44I - _VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1962	I2C_HC_W136 F_LC_V44L - _VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1963	I2C_HC_W136 F_LC_V44L - _VL	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1964	I2C_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1965	I2C_LC_G141	artificial	QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP

	S - VL		GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1966	I2C_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1967	I2C_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1968	I2C_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1969	I2C_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1970	I2C_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1971	I2C_LC_L83S - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1972	I2C_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1973	I2C_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1974	I2C_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1975	I2C_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1976	I2C_LC_V107 A - HCDR1	artificial	KYAMN
1977	I2C_LC_V107 A - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1978	I2C_LC_V107 A - HCDR3	artificial	HGNFGNSYISYWAY
1979	I2C_LC_V107 A - LCDR1	artificial	GSSTGAVTSGNYPN
1980	I2C_LC_V107 A - LCDR2	artificial	GTKFLAP
1981	I2C_LC_V107 A - LCDR3	artificial	ALWYSNRWV
1982	I2C_LC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1983	I2C_LC_V107 A - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1984	I2C_LC_V107 L - HCDR1	artificial	KYAMN
1985	I2C_LC_V107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1986	I2C_LC_V107 L - HCDR3	artificial	HGNFGNSYISYWAY
1987	I2C_LC_V107 L - LCDR1	artificial	GSSTGAVTSGNYPN
1988	I2C_LC_V107 L - LCDR2	artificial	GTKFLAP
1989	I2C_LC_V107 L - LCDR3	artificial	LLWYSNRWV
1990	I2C_LC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1991	I2C_LC_V107 L - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1992	I2C_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1993	I2C_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1994	I2C_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1995	I2C_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1996	I2C_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1997	I2C_LC_V44M - VL	artificial	QTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

1998	I2C_LC_W109 Y - HCDR1	artificial	KYAMN
1999	I2C_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKD
2000	I2C_LC_W109 Y - HCDR3	artificial	HGNFGNSYISYWAY
2001	I2C_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGNYPN
2002	I2C_LC_W109 Y - LCDR2	artificial	GTKFLAP
2003	I2C_LC_W109 Y - LCDR3	artificial	VLYYSNRWV
2004	I2C_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
2005	I2C_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
2006	I2E - HCDR1	artificial	KYAIN
2007	I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2008	I2E - HCDR3	artificial	AGNFGSSYISYWAY
2009	I2E - LCDR1	artificial	GSSTGAVTSGNYPN
2010	I2E - LCDR2	artificial	GTKFLAP
2011	I2E - LCDR3	artificial	VLWYSNRWV
2012	I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWG QGTLVTVSS
2013	I2E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
2014	I2K - HCDR1	artificial	KYAMN
2015	I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
2016	I2K - HCDR3	artificial	NENIGTSYISYWAY
2017	I2K - LCDR1	artificial	GSSTGAVTSGNYPN
2018	I2K - LCDR2	artificial	GTKFLAP
2019	I2K - LCDR3	artificial	VLWYSNRWV
2020	I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWG QGTLVTVSS
2021	I2K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
2022	I2L - HCDR1	artificial	KYAMN
2023	I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2024	I2L - HCDR3	artificial	AGNFGSSYISYFAY
2025	I2L - LCDR1	artificial	GSSTGAVTSGNYPN
2026	I2L - LCDR2	artificial	GTKFLAP
2027	I2L - LCDR3	artificial	VLYYSNRWV
2028	I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWG QGTLVTVSS
2029	I2L - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
2030	I2M - HCDR1	artificial	KYAMN
2031	I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2032	I2M - HCDR3	artificial	AGNFGTSYISYWAY
2033	I2M - LCDR1	artificial	GSSTGAVTSGNYPN
2034	I2M - LCDR2	artificial	GTKFLAP
2035	I2M - LCDR3	artificial	VLWYSNRWV
2036	I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWG QGTLVTVSS
2037	I2M - VL	artificial	QTVVTQEPSTLVSPGGTVTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL

2038	I2M2 - HCDR1	artificial	KYAIN
2039	I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2040	I2M2 - HCDR3	artificial	NANFGTSYISYFAY
2041	I2M2 - LCDR1	artificial	GSSTGAVTSGNYPN
2042	I2M2 - LCDR2	artificial	GTKFLAP
2043	I2M2 - LCDR3	artificial	VLWYSNRWV
2044	I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWG QGTLVTVSS
2045	I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCWLWYSNRWVFGSGTKLTVL
2046	consensus_s equence_1 - HCDR1	artificial	KYAMN
2047	consensus_s equence_1 - HCDR2	artificial	RIRSKYNNYATYYADSVKD
2048	consensus_s equence_1 - HCDR3	artificial	HGNFGNSYJSXWAY
2049	consensus_s equence_1 - LCDR1	artificial	GSSTGAVTSGYYPN
2050	consensus_s equence_1 - LCDR2	artificial	GTKFLAP
2051	consensus_s equence_1 - LCDR3	artificial	ALWYSNRWV
2052	consensus_s equence_1 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYJSXWAYWG QGTLVTVSS
2053	consensus_s equence_1 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
2054	consensus_s equence_2 - HCDR1	artificial	KYAMN
2055	consensus_s equence_2 - HCDR2	artificial	RIRSKYNNYATYYADSVKX
2056	consensus_s equence_2 - HCDR3	artificial	HGNFGNSYJSYWAY
2057	consensus_s equence_2 - LCDR1	artificial	GSSTGAVTSGYYPN
2058	consensus_s equence_2 - LCDR2	artificial	GTKFLAP
2059	consensus_s equence_2 - LCDR3	artificial	ALWYSNRWV
2060	consensus_s equence_2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKXRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYJSYWAYWG QGTLVTVSS
2061	consensus_s equence_2 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWWQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
2062	consensus_s equence_3 - HCDR1	artificial	KYAMN
2063	consensus_s equence_3 - HCDR2	artificial	RIRSKYNNYATYYADSVKX
2064	consensus_s equence_3 - HCDR3	artificial	HGNFGNSYISYWAY
2065	consensus_s equence_3 -	artificial	GSSTGAVTSGYYPN

	LCDR1		
2066	consensus_s equence_3 - LCDR2	artificial	GTKFLAP
2067	consensus_s equence_3 - LCDR3	artificial	ALWYSNRWV
2068	consensus_s equence_3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKXRFITISRDTSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
2069	consensus_s equence_3 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
2070	consensus_s equence_4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDTSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
2071	consensus_s equence_4 - VL	artificial	QTVVTQEPSTLVSPGGTTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2072	BC A7 27- C4-G7 - HCDR1	artificial	NHIIH
2073	BC A7 27- C4-G7 - HCDR2	artificial	YINPYPGYHAYNEKFQG
2074	BC A7 27- C4-G7 - HCDR3	artificial	DGYRDTDVLDY
2075	BC A7 27- C4-G7 - LCDR1	artificial	QASQDISNYLN
2076	BC A7 27- C4-G7 - LCDR2	artificial	YTSRLHT
2077	BC A7 27- C4-G7 - LCDR3	artificial	QQGNTLPWT
2078	BC A7 27- C4-G7 - VH	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTHNIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSS
2079	BC A7 27- C4-G7 - VL	artificial	DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDYATYYCQQGNTLPWTFGGGTKEIK
2080	BC A7 27- C4-G7 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTHNIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSS
2081	BC A7 27- C4-G7 CC - VL	artificial	DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDYATYYCQQGNTLPWTFGGGTKEIK
2082	BC A7 27- C4-G7 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDYATYYCQQGNTLPWTFGGGTKEIK
2083	BC A7 27- C4-G7 EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDYATYYCQQGNTLPWTFGGGTKEIK
2084	BC A7 27- C4-G7X I2C - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTHNIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFGSGSGTDFTFTISSLEPEDYATYYCQQGNTLPW TFGGGTKEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDTSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGSGGGSGTQTVVTQEPSTLVSPGGT VTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2085	BC A7 27- C4-G7X I2E - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTHNIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFGSGSGTDFTFTISSLEPEDYATYYCQQGNTLPW TFGGGTKEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDTSKNTVYLQMNNLKTEDTAVYYCA RAGNFGSSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGSGGGSGTQTVVTQEPSTLVSPGGT VTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2086	BC A7 27- C4-G7X I2K - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTHNIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFGSGSGTDFTFTISSLEPEDYATYYCQQGNTLPW

			TFQGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVVYCV RNIENIGTSYISYWAYWQGQTLVTVSSGGGGSGGGSGGGGSQTVVTQEPISLTVSPGGT VTITCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2087	BC A7 27- C4-G7X I2L - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHIH IHWVRQAPQGQLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMLSSLRSEDTAVYYCARDGYRDTDVLVDYWGQGT LVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFSGSGSGTDFTFTISSLEPEDATYYCQGGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVVYCV RAGNFGSSYISYFAYWQGQTLVTVSSGGGGSGGGSGGGGSQTVVTQEPISLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAAL TLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
2088	BC A7 27- C4-G7X I2M - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHIH IHWVRQAPQGQLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMLSSLRSEDTAVYYCARDGYRDTDVLVDYWGQGT LVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFSGSGSGTDFTFTISSLEPEDATYYCQGGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVVYCV RAGNFGTSYISYFAYWQGQTLVTVSSGGGGSGGGSGGGGSQTVVTQEPISLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2089	BC A7 27- C4-G7X I2M2 - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHIH IHWVRQAPQGQLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMLSSLRSEDTAVYYCARDGYRDTDVLVDYWGQGT LVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFSGSGSGTDFTFTISSLEPEDATYYCQGGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVVYCV RNIANFGTSYISYFAYWQGQTLVTVSSGGGGSGGGSGGGGSQTVVTQEPISLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2090	BC A7 27- C4-G7 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHIH IHWVRQAPQGQLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMLSSLRSEDTAVYYCARDGYRDTDVLVDYWGQGT LVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFSGSGSGTDFTFTISSLEPEDATYYCQGGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVVYCV RHGNFGNSYISYWAYWQGQTLVTVSSGGGGSGGGSGGGGSQTVVTQEPISLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGKTCLTVLGGGGDKHTHCPCPAPELLGGPSV FLFPKPKPDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDK SRWQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGGS GGGSGDKHTHCPCPAPELLGGPSVFLFPKPKPDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNNAKTPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NYYKTTTPVLDSDGGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNNHYTQKSLSLSPGK
2091	BC A7 27- C4-G7 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHIH IHWVRQAPQGQLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMLSSLRSEDTAVYYCARDGYRDTDVLVDYWGQGT LVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFSGSGSGTDFTFTISSLEPEDATYYCQGGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVYYCA RAGNFGSSYISYWAYWQGQTLVTVSSGGGGSGGGSGGGGSQTVVTQEPISLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHCPCPAPELLGGPSV FLFPKPKPDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDK SRWQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGGS GGGSGDKHTHCPCPAPELLGGPSVFLFPKPKPDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNNAKTPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NYYKTTTPVLDSDGGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNNHYTQKSLSLSPGK
2092	BC A7 27- C4-G7 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHIH IHWVRQAPQGQLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMLSSLRSEDTAVYYCARDGYRDTDVLVDYWGQGT LVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSPRFSGSGSGTDFTFTISSLEPEDATYYCQGGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVVYCV RNIENIGTSYISYWAYWQGQTLVTVSSGGGGSGGGSGGGGSQTVVTQEPISLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHCPCPAPELLGGPSV FLFPKPKPDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDK SRWQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGGS GGGSGDKHTHCPCPAPELLGGPSVFLFPKPKPDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNNAKTPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NYYKTTTPVLDSDGGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNNHYTQKSLSLSPGK

			EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSKDTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTI SAKKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2093	BC A7 27- C4-G7 CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFNTHIIHWVRQAPGQCLEWMGYINPYPGYH AYNEKFPQGRATMTSDTSTSTVYMESSLRSSEDTAVYYCARDGYRDTDVLDYWGQGT LVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSLRHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGMEWVARIRSKYNNYATYYADAVKDRTISRDDSNTLYLQMNMLKTEDTAVYYCV RAGNFGTSYISYFAYWGQGTTLTVSSGGGSGGGGSGGGGSGGGGSGQTVVTQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWIKKPKQAPRGLIGGTKFLAPGTPARFSGSLEGGKAA TLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSKDTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTI SAKKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2094	BC A7 27- C4-G7 CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFNTHIIHWVRQAPGQCLEWMGYINPYPGYH AYNEKFPQGRATMTSDTSTSTVYMESSLRSSEDTAVYYCARDGYRDTDVLDYWGQGT LVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSLRHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGMEWVARIRSKYNNYATYYADAVKDRTISRDDSNTLYLQMNMLKTEDTAVYYCV RAGNFGTSYISYFAYWGQGTTLTVSSGGGSGGGGSGGGGSGGGGSGQTVVTQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPKQAPRGLIGGTKFLAPGTPARFSGSLEGGKAA TLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSKDTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTI SAKKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2095	BC A7 27- C4-G7 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFNTHIIHWVRQAPGQCLEWMGYINPYPGYH AYNEKFPQGRATMTSDTSTSTVYMESSLRSSEDTAVYYCARDGYRDTDVLDYWGQGT LVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSLRHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAP GKGLEWVARIRSKYNNYATYYADAVKDRTISRDDSNTAYLQMNMLKTEDTAVYYCV RNANFGTSYISYFAYWGQGTTLTVSSGGGSGGGGSGGGGSGGGGSGQTVVTQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPKQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA TLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSKDTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTI SAKKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2096	CD123 24- B4-f NK CC - HCDR1	artificial	HYAMS
2097	CD123 24- B4-f NK CC - HCDR2	artificial	AVSGGGDKTLYADAVKG
2098	CD123 24- B4-f NK CC - HCDR3	artificial	LRGFYYGMDV
2099	CD123 24- B4-f NK CC - LCDR1	artificial	RSSQSLHNSKNKYLD
2100	CD123 24- B4-f NK CC - LCDR2	artificial	LGSNRAS
2101	CD123 24- B4-f NK CC - LCDR3	artificial	MQALQTPPIT
2102	CD123 24- B4-f NK CC	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSASVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRRAEDTAIYYCARLGRFYFGMDVWGQGTIV

	- VH		VSS
2103	CD123 24- B4-f NK CC - VL	artificial	DIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDWYLQKPGQSPQLLIYLGSN RASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQTPPITFGCGTRLEIK
2104	CD123 24- B4-f NK CC EI GQ - VL	artificial	EIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDWYLQKPGQSPQLLIYLGSN RASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQTPPITFGCGTRLEIK
2105	CD123 24- B4-f NK CC x I2C x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWWSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLRGFYGMVDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNKLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTILVTSSGGGSGGGGSGGGGSGTQVTVTQEPFLTVS PGGTVTITCGSSTGAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTAPARFSGSLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEE QYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSL SPGK
2106	CD123 24- B4-f NK CC x I2E x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWWSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLRGFYGMVDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINNWV RQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAV YYCARAGNFGSSYISYWAYWGQGTILVTSSGGGSGGGGSGGGGSGTQVTVTQEPFLTVS PGGTVTITCGSSTGAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTAPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEE QYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSL SPGK
2107	CD123 24- B4-f NK CC x I2K x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWWSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLRGFYGMVDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDTAV YYCVRNENIGTSYISYWAYWGQGTILVTSSGGGSGGGGSGGGGSGTQVTVTQEPFLTVS PGGTVTITCGSSTGAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTAPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEE QYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSL SPGK
2108	CD123 24- B4-f NK CC x I2L x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWWSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLRGFYGMVDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAV YYCVRAGNFGSSYISYFAYWGQGTILVTSSGGGSGGGGSGGGGSGTQVTVTQEPFLTVS PGGTVTITCGSSTGAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTAPARFSGSLGG KAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEE QYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG

			QPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFSQVMSHEALHNYHTQKSLSLSPGK
2109	CD123 24- B4-f NK CC x I2M x scFc - Full Sequence	artificial	EVQLLESGGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSASVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLGRFYGMVWQGGTTVT VSSGGGGSGGGSGGGSDIVLTQSPSLPVTPEEPASISCRSSQSLHNSKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLTKISRVEAEDVGYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWV RQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAV YYCVRAGNFGTSYISYWAYWGQGTLLVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPKPGQAPRGLIGGTFKFLAPGTTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLG GPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKL TVDKSRWQQGNVFSQVMSHEALHNYHTQKSLSLSPGKGGGGSGGGSGGGSGGGSGG GGSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFSQVMSHEALHNYHTQKSLSL SPGK
2110	CD123 24- B4-f NK CC x I2M2 x scFc - Full Sequence	artificial	EVQLLESGGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSASVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLGRFYGMVWQGGTTVT VSSGGGGSGGGSGGGSDIVLTQSPSLPVTPEEPASISCRSSQSLHNSKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLTKISRVEAEDVGYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWV REAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRNANFGTSYISYFAYWGQGTLLVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPKPGQAPRGLIGGTFKFLAPGTTPARFSGSLG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLG GPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKL TVDKSRWQQGNVFSQVMSHEALHNYHTQKSLSLSPGKGGGGSGGGSGGGSGGGSGG GGSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHED DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFSQVMSHEALHNYHTQKSLSL SPGK
2111	CD19 97- G1RE-C2 LH CC - HCDR1	artificial	SYGMH
2112	CD19 97- G1RE-C2 LH CC - HCDR2	artificial	VISYEGSNKYAESVKG
2113	CD19 97- G1RE-C2 LH CC - HCDR3	artificial	DRGTIFGNYGLEV
2114	CD19 97- G1RE-C2 LH CC - LCDR1	artificial	RSSQSLHKNFNYLD
2115	CD19 97- G1RE-C2 LH CC - LCDR2	artificial	LGSNRAS
2116	CD19 97- G1RE-C2 LH CC - LCDR3	artificial	MQALQTPFT
2117	CD19 97- G1RE-C2 LH CC - VH	artificial	QVQLVESGGGVVQPGSRSLRLSCAASGFTSSSYGMHWVRQAPGKCLEWVAVISYEGSNK YAESVKGRTISRDNKNTLYLQMNSLRDEDTAVYYCARDRTIFGNYGLEVWGGQT TVTVSS
2118	CD19 97- G1RE-C2 LH CC - VL	artificial	DIVMTQSPSLSPVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLTKISRVEAEDVGYYCMQALQTPFTFGCGTKVDIK
2119	CD19 97- G1RE-C2 LH CC EI GQ - VL	artificial	EIVMTQSPSLSPVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLTKISRVEAEDVGYYCMQALQTPFTFGCGTKVDIK
2120	CD19 97- G1RE-C2 LH CC x I2C x scFc - Full Sequence	artificial	DIVMTQSPSLSPVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLTKISRVEAEDVGYYCMQALQTPFTFGCGTKVDIKGGG SGGGSGGGGSGVQLVESGGGVVQPGSRSLRLSCAASGFTSSSYGMHWVRQAPGKCLEW VAVISYEGSNKYAESVKGRTISRDNKNTLYLQMNSLRDEDTAVYYCARDRTIFG NYGLEVWGGQTTVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLLVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTL VSPGGTITCGSSTGAVTSGNYPNWVQKPKPGQAPRGLIGGTFKFLAPGTTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGSGTKLTVLGGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYIT

			LPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLSDSGSFFLYS KLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG SGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWES NGQPENNYKTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSL SLSPGK
2121	CD19 97- G1RE-C2 LH CC x I2E x scFc - Full Sequence	artificial	DIVMTQSPSLSPVISGEPASISCRSSQSLHKNFAFNLYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGSGGGSQVLVESGGGVVQPGRSLRLSCAASGFTSSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDNKNTLYLQMNLSLRDEDTAVYYCARDRTGIFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDT AVYYCARAGNFGSSYISYWAYWQGQTLTVSSSGGGSGGGSGGGSGGGSQTVVTQEPISLT VSPGGTITITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPEL LGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLSDSGSFFLYS KLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG SGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWES NGQPENNYKTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSL SLSPGK
2122	CD19 97- G1RE-C2 LH CC x I2K x scFc - Full Sequence	artificial	DIVMTQSPSLSPVISGEPASISCRSSQSLHKNFAFNLYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGSGGGSQVLVESGGGVVQPGRSLRLSCAASGFTSSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDNKNTLYLQMNLSLRDEDTAVYYCARDRTGIFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDT AVYYCVRNENIGTSYISYWAYWQGQTLTVSSSGGGSGGGSGGGSGGGSQTVVTQEPISLT VSPGGTITITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPEL LGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLSDSGSFFLYS KLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG SGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWES NGQPENNYKTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSL SLSPGK
2123	CD19 97- G1RE-C2 LH CC x I2L x scFc - Full Sequence	artificial	DIVMTQSPSLSPVISGEPASISCRSSQSLHKNFAFNLYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGSGGGSQVLVESGGGVVQPGRSLRLSCAASGFTSSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDNKNTLYLQMNLSLRDEDTAVYYCARDRTGIFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDT AVYYCVRAGNFGSSYISYFAYWQGQTLTVSSSGGGSGGGSGGGSGGGSQTVVTQEPISLT VSPGGTITITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPEL LGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLSDSGSFFLYS KLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG SGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWES NGQPENNYKTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSL SLSPGK
2124	CD19 97- G1RE-C2 LH CC x I2M x scFc - Full Sequence	artificial	DIVMTQSPSLSPVISGEPASISCRSSQSLHKNFAFNLYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGSGGGSQVLVESGGGVVQPGRSLRLSCAASGFTSSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDNKNTLYLQMNLSLRDEDTAVYYCARDRTGIFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDT AVYYCVRAGNFGTSYISYWAYWQGQTLTVSSSGGGSGGGSGGGSGGGSQTVVTQEPISLT VSPGGTITITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPEL LGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLSDSGSFFLYS KLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG SGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIAVEWES NGQPENNYKTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSL SLSPGK

			NGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSL SLSPGK
2125	CD19 97- G1RE-C2 LH CC x I2M2 x scFc - Full Sequence	artificial	DIVMTQSPSLPVSISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGGSGVQLVSESGGVVQPGRLRLSCAASGFTSSYGMHWVRQAPGKCLEW VAVISYEGSNKYAESVKGRFTISRDNKNTLYLQMNSLRDEDTAVYYCARDRTIFG NYGLEVWQGTITVTVSSSGGGSEVQLVSESGGLVQPGGSLKLSCAASGFTFNKYAIN WVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNLLKTEDT AVYYCVRNANFGTSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGGSGTAVVTVQEP SLTVSPGGTIVLTGSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQQDLNKGKEYCKVSNKALPAPI EKTISKAKGQPREPQVY TLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGG SGGGSGGGGSGDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQQDLNKGKEYCKV SNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSL SLSPGK
2126	CD20 99-E5 CC - HCDR1	artificial	SYWMH
2127	CD20 99-E5 CC - HCDR2	artificial	YITPSTGYTEYNQKFKG
2128	CD20 99-E5 CC - HCDR3	artificial	VHDYDRA MEY
2129	CD20 99-E5 CC - LCDR1	artificial	KASQDINKYIA
2130	CD20 99-E5 CC - LCDR2	artificial	YTSTLQP
2131	CD20 99-E5 CC - LCDR3	artificial	LQYASYPFT
2132	CD20 99-E5 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRDKSTSTVYMESSLTSEDYAVYYCARVHDYDRA MEYWGQGTITV VSS
2133	CD20 99-E5 CC - VL	artificial	DIQMTQSPSSLSASVGRVITITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGV PSRFGSGSGTDFTFTISSSLQPEDIAATYYCLQYASYPFTFGCGTRLEIK
2134	CD20 99-E5 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGRVITITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGV PSRFGSGSGTDFTFTISSSLQPEDIAATYYCLQYASYPFTFGCGTRLEIK
2135	CD20 99-E5 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRDKSTSTVYMESSLTSEDYAVYYCARVHDYDRA MEYWGQGTITV VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGRVITITCKASQDINKYIAWYQQK PKGPKLLIYYTSTLQPGVPSRFGSGSGTDFTFTISSSLQPEDIAATYYCLQYASYPFTF GCGTRLEIKSGGGGSEVQLVSESGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDYAVYYCVRH GNFGNSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTAVVTVQEP SLTVSPGGTIVLTGSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL LGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGYSTYRCVSVLTVLHQQDLNKGKEYCKVSNKALPAPI EKTISKAKGQPREPQVY TLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGSGDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKF NMYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQQDLNKGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2136	CD20 99-E5 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRDKSTSTVYMESSLTSEDYAVYYCARVHDYDRA MEYWGQGTITV VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGRVITITCKASQDINKYIAWYQQK PKGPKLLIYYTSTLQPGVPSRFGSGSGTDFTFTISSSLQPEDIAATYYCLQYASYPFTF GCGTRLEIKSGGGGSEVQLVSESGGLVQPGGSLKLSCAASGFTFNKYAINNWRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNLLKTEDYAVYYCARA GNFGSSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTAVVTVQEP SLTVSPGGTIVLTGSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL SGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGYSTYRCVSVLTVLHQQDLNKGKEYCKVSNKALPAPI EKTISKAKGQPREPQVY TLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGSGDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKF NMYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQQDLNKGKEYCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2137	CD20 99-E5 CC x I2K x scFc - Full	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRDKSTSTVYMESSLTSEDYAVYYCARVHDYDRA MEYWGQGTITV VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGRVITITCKASQDINKYIAWYQQK

	Sequence		GKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPTTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVNRN ENIGTSYISYWAYWQGTLVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2138	CD20 99-E5 CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYMMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRDKSTSTVYMESSLTSEDNAVYYCARVHDYDRAMEYWGQGTIVT VSSGGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPTTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRA GNFGTSYISYFAYWQGTLVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2139	CD20 99-E5 CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYMMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRDKSTSTVYMESSLTSEDNAVYYCARVHDYDRAMEYWGQGTIVT VSSGGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPTTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRA GNFGTSYISYFAYWQGTLVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2140	CD20 99-E5 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYMMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRDKSTSTVYMESSLTSEDNAVYYCARVHDYDRAMEYWGQGTIVT VSSGGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPTTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVNRN ANFGTSYISYFAYWQGTLVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2141	CD22 28- B7N65S CC - HCDR1	artificial	SYGIS
2142	CD22 28- B7N65S CC - HCDR2	artificial	WISAYSGNAIYAQKLQG
2143	CD22 28- B7N65S CC - HCDR3	artificial	DPDYSGSGSYSDY
2144	CD22 28- B7N65S CC - LCDR1	artificial	RASQSVSSNLA

2145	CD22 28-B7N65S CC - LCDR2	artificial	GASSRAT
2146	CD22 28-B7N65S CC - LCDR3	artificial	QQYHSWPLLT
2147	CD22 28-B7N65S CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYVSGSGSYSDYWGQGT LVTVSS
2148	CD22 28-B7N65S CC - VL	artificial	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWPLLTFCGCTKVEIK
2149	CD22 28-B7N65S CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYVSGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFNSYI SYWAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCCPPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSQSVMHAEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGTQVVTQEPSLTVSPG GSGGGGDKTHTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMHAEALHNNHYTQKSLSLSP GK
2150	CD22 28-B7N65S CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYVSGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWRQ APGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYY CARAGNFGSSYI SYWAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCCPPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSQSVMHAEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GSGGGGDKTHTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMHAEALHNNHYTQKSLSLSP GK
2151	CD22 28-B7N65S CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYVSGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQ APGKGLEWVARIRSKYNNYATYYAEAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYY CVRNENIGTSYI SYWAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCCPPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSQSVMHAEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GSGGGGDKTHTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMHAEALHNNHYTQKSLSLSP GK
2152	CD22 28-B7N65S CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYVSGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQ APGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYY CVRAGNFGSSYI SYFAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSLTVSPG GTVTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCCPPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPS

			REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GSGGGGSKTHTCPPCPAPELLGPPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDNLNGKEYCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSP GK
2153	CD22 28-B7 N65S CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMMWISAYSNGA IYAQKLQGRVTMRDSTSTAYMELRSLRSDDTAVYYCARDPDYVSGSYSDYWGQGT LVTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYCCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNVRQ APGKGMWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYY CVRAGNFGTSYISYWAYWGQGT LVTVSSGGGSGGGGSGGGGSGT VVTQEP SLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLGPP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GYSTYRCVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GSGGGGSKTHTCPPCPAPELLGPPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDNLNGKEYCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSP GK
2154	CD22 28-B7 N65S CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMMWISAYSNGA IYAQKLQGRVTMRDSTSTAYMELRSLRSDDTAVYYCARDPDYVSGSYSDYWGQGT LVTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYCCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRE APGKGLEWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYY CVRNANFGTSYISYFAYWGQGT LVTVSSGGGSGGGGSGGGGSGT VVTQEP SLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLGPP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GYSTYRCVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GSGGGGSKTHTCPPCPAPELLGPPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDNLNGKEYCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSP GK
2155	CD33 E11 - HCDR1	artificial	NYGMN
2156	CD33 E11 - HCDR2	artificial	WINTYTGEPTYADKFGQ
2157	CD33 E11 - HCDR3	artificial	WSWSDGYVYFDY
2158	CD33 E11 - LCDR1	artificial	KSSQSVLDSSTNKNLSA
2159	CD33 E11 - LCDR2	artificial	WASTRES
2160	CD33 E11 - LCDR3	artificial	QQSAHFPIIT
2161	CD33 E11 - VH	artificial	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWKQAPGQGLEWMMWINTYTGE TYADKFGQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSS
2162	CD33 E11 - VL	artificial	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQAHPFITFGQGTREIK
2163	CD33 E11 CC - VH	artificial	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWKQAPGQCLEWMMWINTYTGE TYADKFGQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSS
2164	CD33 E11 CC - VL	artificial	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQAHPFITFGQGTREIK
2165	CD33 E11 CC EI GQ - VL	artificial	EIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQAHPFITFGQGTREIK
2166	CD33 E11 EI GQ - VL	artificial	EIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQAHPFITFGQGTREIK
2167	E11 x I2C - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWKQAPGQGLEWMMWINTYTGE TYADKFGQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHPFITFGQGTREIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAM NWRQAPGKGLEWVARIIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTED TAVYCVRHGNGFNSYISYWAYWGQGT LVTVSSGGGSGGGGSGGGGSGT VVTQEP SL TVSPGGT VTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL

			LGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2168	E11 x I2E - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYTFTNYGMNHWVKQAPQGGLLEWGWINTYTGPETYADKFQGRVTRMTTDTISTSTAYMEIRNLGGDDTAVYYCARWSWSGDYVYVFDYWGGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGI PDRFSGSGSGTDFTLTIDSPQEDSATYYCQSAHFPITFTGQGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAIVNWRQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDSKNTVLYQMNLKTEDTAVYYCVRAGNFGSSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGSGTQVTVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2169	E11 x I2K - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYTFTNYGMNHWVKQAPQGGLLEWGWINTYTGPETYADKFQGRVTRMTTDTISTSTAYMEIRNLGGDDTAVYYCARWSWSGDYVYVFDYWGGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGI PDRFSGSGSGTDFTLTIDSPQEDSATYYCQSAHFPITFTGQGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLIEWVARIRSKYNNYATYYAAEVKGRFTISRDSKNTVLYQMNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGSGTQVTVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2170	E11 x I2L - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYTFTNYGMNHWVKQAPQGGLLEWGWINTYTGPETYADKFQGRVTRMTTDTISTSTAYMEIRNLGGDDTAVYYCARWSWSGDYVYVFDYWGGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGI PDRFSGSGSGTDFTLTIDSPQEDSATYYCQSAHFPITFTGQGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDSKNTVLYQMNLKTEDTAVYYCVRNENFGTSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGSGTQVTVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSEGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2171	E11 x I2M - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYTFTNYGMNHWVKQAPQGGLLEWGWINTYTGPETYADKFQGRVTRMTTDTISTSTAYMEIRNLGGDDTAVYYCARWSWSGDYVYVFDYWGGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGI PDRFSGSGSGTDFTLTIDSPQEDSATYYCQSAHFPITFTGQGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDSKNTVLYQMNLKTEDTAVYYCVRNENFGTSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGSGTQVTVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2172	E11 x I2M2 - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYTFTNYGMNHWVKQAPQGGLLEWGWINTYTGPETYADKFQGRVTRMTTDTISTSTAYMEIRNLGGDDTAVYYCARWSWSGDYVYVFDYWGGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGI PDRFSGSGSGTDFTLTIDSPQEDSATYYCQSAHFPITFTGQGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAIVNWRQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDSKNTVLYQMNLKTEDTAVYYCVRNENFGTSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGSGTQVTVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2173	CD33 E11 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYTFTNYGMNHWVKQAPQGGLLEWGWINTYTGPETYADKFQGRVTRMTTDTISTSTAYMEIRNLGGDDTAVYYCARWSWSGDYVYVFDYWGGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGI PDRFSGSGSGTDFTLTIDSPQEDSATYYCQSAHFPITFTGCGTRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAIVNWRQAPGKGLIEWVARIRSKYNNYATYYADSVKDRFTISRDSKNTVLYQMNLKTEDTAVYYCVRHNGFNSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGSGTQVTVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGGDKHTHCPPCPAELGGPSVLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQKSLSLSPGKGGGSGGGGSGGGSGSGGGGSGGGGSDKHTHCPPCPAPELLGGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQKSLSLSPGK
2174	CD33 E11 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYTFTNYGMNHWVKQAPQGGLLEWGWINTYTGPETYADKFQGRVTRMTTDTISTSTAYMEIRNLGGDDTAVYYCARWSWSGDYVYVFDYWGGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGI PDRFSGSGSGTDFTLTIDSPQEDSATYYCQSAHFPITFTGCGTRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAIVNWRQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDSKNTVLYQMNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGLVTVSSGGGGSGGGGSGGGSGTQVTVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGGDKHTHCPPCPAELGGPSVLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQKSLSLSPGK

			SGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK
2175	CD33 E11 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYFTFTNYGMNWKQAPGCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMMNLKTED TAVYVCVRNENIGTSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQVTVQEP SLTVSPGGTITICGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG SGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK
2176	CD33 E11 CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYFTFTNYGMNWKQAPGCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMMNLKTED TAVYVCVRNENIGTSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQVTVQEP SLTVSPGGTITICGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKHTHTCP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG SGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK
2177	CD33 E11 CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYFTFTNYGMNWKQAPGCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMMNLKTED TAVYVCVRNENIGTSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQVTVQEP SLTVSPGGTITICGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG SGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK
2178	CD33 E11 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYFTFTNYGMNWKQAPGCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMMNLKTED TAVYVCVRNANFGTSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSGTQVTVQEP SLTVSPGGTITICGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG SGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK

2179	CD70 1 C7D CC - HCDR1	artificial	TYAMS
2180	CD70 1 C7D CC - HCDR2	artificial	AISGSGGRTFYAESVEG
2181	CD70 1 C7D CC - HCDR3	artificial	HDYSNYPYFDY
2182	CD70 1 C7D CC - LCDR1	artificial	RASQSVRSTYLA
2183	CD70 1 C7D CC - LCDR2	artificial	GASSRAT
2184	CD70 1 C7D CC - LCDR3	artificial	QQYGDLPFT
2185	CD70 1 C7D CC - VH	artificial	EVQLLESgggmVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWVSAISGSGGRT FYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTILV TVSS
2186	CD70 1 C7D CC - VL	artificial	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLA WYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIK
2187	CD70 1 C7D CC x I2C x scFc - Full Sequence	artificial	EVQLLESgggmVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWVSAISGSGGRT FYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTILV TVSSGGGGSGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLA WYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPF TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMN LKTEDTAVYYCV RHGNFGNSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDK SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2188	CD70 1 C7D CC x I2E x scFc - Full Sequence	artificial	EVQLLESgggmVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWVSAISGSGGRT FYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTILV TVSSGGGGSGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLA WYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPF TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDS KNTVYLQMN LKTEDTAVYYCA RAGNFGSSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDK SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2189	CD70 1 C7D CC x I2K x scFc - Full Sequence	artificial	EVQLLESgggmVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWVSAISGSGGRT FYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTILV TVSSGGGGSGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLA WYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPF TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDS KNTVYLQMN LKTEDTAVYYCV RNENIGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDK SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2190	CD70 1 C7D CC x I2L x scFc - Full Sequence	artificial	EVQLLESgggmVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWVSAISGSGGRT FYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTILV TVSSGGGGSGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLA WYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPF TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDS KNTLYLQMN LKTEDTAVYYCV RAGNFGSSYISYFAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV

200

			SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGG GGSGGGSDKTHTCPPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2202	CH19 2G6.007 CCx I2C x scFc delGK - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNK YYAESVKDRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYGYGMDVWG QGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYSW YQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGGTCLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNNKYAMNVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVY YCVRHGNFGNSYISYWAYWGGTTLTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGTITVITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGT PARFSGSLSGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGGKTCLTVLGGGGDKTHTCPPCAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGG GGSGGGSDKTHTCPPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2203	CH19 2G6.007 CCx I2E x scFc - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNK YYAESVKDRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYGYGMDVWG QGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYSW YQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGGTCLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNNKYAMNVR QAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTEDTAVY YCARAGNFGSSYISYWAYWGGTTLTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGTITVITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGT PARFSGSLSGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGSGTCLTVLGGGGDKTHTCPPCAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGG GGSGGGSDKTHTCPPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2204	CH19 2G6.007 CCx I2E x scFc delGK - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNK YYAESVKDRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYGYGMDVWG QGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYSW YQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGGTCLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNNKYAMNVR QAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTEDTAVY YCARAGNFGSSYISYWAYWGGTTLTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGTITVITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGT PARFSGSLSGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGSGTCLTVLGGGGDKTHTCPPCAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGG GGSGGGSDKTHTCPPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2205	CH19 2G6.007 CCx I2K x scFc - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNK YYAESVKDRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYGYGMDVWG QGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYSW YQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGGTCLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNNKYAMNVR QAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNLLKTEDTAVY YCVRNENIGTSYISYWAYWGGTTLTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGTITVITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGT PARFSGSLSGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGSGTCLTVLGGGGDKTHTCPPCAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGG GGSGGGSDKTHTCPPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ

			PENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2206	CH19 2G6.007 CCx I2K x scFc delGK - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTSSYGMHVRQAPGKCLEWVAFIWEYSNKK YYAESVKDRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTTVTVSSGGGGGGGGGGGGSSYELTQPPSVSVSPGQTASITCSGDRLEGEKYSW YQQRPGQSPLLVIYQDTRKPSGI PERFGSGNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKLEWVARIIRSKYNNYATYYAEAVKGRFTISRDDSKNTLYLQMNLSLRAEDTAVYY YCVRNENIGTSYISYWAYWGQGLTVTVSSGGGGGGGGGGGGGGGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGG SGGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2207	CH19 2G6.007 CCx I2L x scFc - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTSSYGMHVRQAPGKCLEWVAFIWEYSNKK YYAESVKDRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTTVTVSSGGGGGGGGGGGGSSYELTQPPSVSVSPGQTASITCSGDRLEGEKYSW YQQRPGQSPLLVIYQDTRKPSGI PERFGSGNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKMEWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNLSLRAEDTAVYY YCVRAGNFGSSYISYWAYWGQGLTVTVSSGGGGGGGGGGGGGGGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLEGGK AALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG GGGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2208	CH19 2G6.007 CCx I2L x scFc delGK - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTSSYGMHVRQAPGKCLEWVAFIWEYSNKK YYAESVKDRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTTVTVSSGGGGGGGGGGGGSSYELTQPPSVSVSPGQTASITCSGDRLEGEKYSW YQQRPGQSPLLVIYQDTRKPSGI PERFGSGNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKMEWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNLSLRAEDTAVYY YCVRAGNFGSSYISYWAYWGQGLTVTVSSGGGGGGGGGGGGGGGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLEGGK AALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGG SGGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2209	CH19 2G6.007 CCx I2M x scFc - Full Sequence	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTSSYGMHVRQAPGKCLEWVAFIWEYSNKK YYAESVKDRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTTVTVSSGGGGGGGGGGGGSSYELTQPPSVSVSPGQTASITCSGDRLEGEKYSW YQQRPGQSPLLVIYQDTRKPSGI PERFGSGNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKMEWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNLSLRAEDTAVYY YCVRAGNFGTSYISYWAYWGQGLTVTVSSGGGGGGGGGGGGGGGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG GGGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2210	CH19 2G6.007 CCx I2M x scFc	artificial	QVQLVESGGGVQPGGSLRLSCAASGFTSSYGMHVRQAPGKCLEWVAFIWEYSNKK YYAESVKDRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTTVTVSSGGGGGGGGGGGGSSYELTQPPSVSVSPGQTASITCSGDRLEGEKYSW

	delGK - Full Sequence		YQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWES STVVFGCGTKLTVLSGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNFKYAMNWVR QAPGKGMEWVARIRSKYNNYATYYADAVKDRTTISRDDSKNTLYLQMNMLKTEDTAVY YCVVRNFGTSTYISYWAYWGQGTTLTVTSGGGGSGGGGSGGGGSGQTVVVQEPSLTVSP GGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGK AALTLTSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCTPPCPAPPELLGG PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP SREEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVPLDSGGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGSGDKTHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVPLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPK
2211	CH19 2G6.007 CCx I2M2 x scFc - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGTFSSYGMHWRVQAPGKCLEWVAFIWEYSNKK YYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYYGMDVWG QGTTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGKEYTSW YQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWES STVVFGCGTKLTVLSGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNFKYAINWVR EAPGKGLEWVARIRSKYNNYATYYADAVKDRTTISRDDSKNTAYLQMNMLKTEDTAVY YCVVRNFGTSTYISYFAYWGQGTTLTVTSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG GGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKK AALTLTSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCTPPCPAPPELLGG PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP SREEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVPLDSGGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GGSGGGSGDKTHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVPLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2212	CH19 2G6.007 CCx I2M2 x scFc delGK - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGTFSSYGMHWRVQAPGKCLEWVAFIWEYSNKK YYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYYGMDVWG QGTTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGKEYTSW YQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWES STVVFGCGTKLTVLSGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNFKYAINWVR EAPGKGLEWVARIRSKYNNYATYYADAVKDRTTISRDDSKNTAYLQMNMLKTEDTAVY YCVVRNFGTSTYISYFAYWGQGTTLTVTSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG GGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKK AALTLTSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCTPPCPAPPELLGG PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP SREEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVPLDSGGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGSGDKTHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVPLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2213	CH3 15-E11 CC - HCDR1	artificial	NYWMN
2214	CH3 15-E11 CC - HCDR2	artificial	NIAYGVKGTNYNQKFQG
2215	CH3 15-E11 CC - HCDR3	artificial	RYFYVM DY
2216	CH3 15-E11 CC - LCDR1	artificial	RASQDISNYLN
2217	CH3 15-E11 CC - LCDR2	artificial	YTSRLHS
2218	CH3 15-E11 CC - LCDR3	artificial	VQYAQFPLT
2219	CH3 15-E11 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYWMNWVRQAPGQCLEWMGNIA YGVKGT NYNQKFGQVRMTVDTSSTAYMELSRRLSDDTAVYYCATRYFYVM DYWGQGTTLTVTS S
2220	CH3 15-E11 CC - VL	artificial	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPKGVKPLLIYYTSRLHSGV PSRFSGSGSGTDFTLTITSLQPEDVATYYCVQYAQFPLTFGCCTKVEIK
2221	CH3 15-E11 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPKGVKPLLIYYTSRLHSGV PSRFSGSGSGTDFTLTITSLQPEDVATYYCVQYAQFPLTFGCCTKVEIK
2222	CH3 G8A 6- B12 - HCDR1	artificial	SYPIN
2223	CH3 G8A 6- B12 - HCDR2	artificial	VIWTGGGTNYASSVKG
2224	CH3 G8A 6- B12 - HCDR3	artificial	SRGVYDFDGRGAMDY

2225	CH3 G8A 6-B12 - LCDR1	artificial	KSSQSLLYSSNQKNYFA
2226	CH3 G8A 6-B12 - LCDR2	artificial	WASTRES
2227	CH3 G8A 6-B12 - LCDR3	artificial	QQYYSYPYT
2228	CH3 G8A 6-B12 - VH	artificial	EVQLLESQGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLEWVGVIWTGGGTN YASSVKGRFTISRDNKNTVYLQMNLSRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLVTVSS
2229	CH3 G8A 6-B12 - VL	artificial	DIVMTQSPDLSAVSLGERATINCKSSQSLLYSSNQKNYFAWYQQKPGQPPKLLIYWAS TRESGVDRFSGSGSGTDFTLTISSLQAEADVAVYYCQQYYSYPYTFGQGTKEIK
2230	CH3 G8A 6-B12 EI GQ - VL	artificial	EIVMTQSPDLSAVSLGERATINCKSSQSLLYSSNQKNYFAWYQQKPGQPPKLLIYWAS TRESGVDRFSGSGSGTDFTLTISSLQAEADVAVYYCQQYYSYPYTFGQGTKEIK
2231	CH3 R170R CC - HCDR1	artificial	SYWMH
2232	CH3 R170R CC - HCDR2	artificial	KIDPSDDYTNYNQKVKG
2233	CH3 R170R CC - HCDR3	artificial	WDYSHFDV
2234	CH3 R170R CC - LCDR1	artificial	RASSSVSYMH
2235	CH3 R170R CC - LCDR2	artificial	GTSNLVS
2236	CH3 R170R CC - LCDR3	artificial	QQWSSYPLT
2237	CH3 R170R CC - VH	artificial	EVQLLESQGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPSDDYT NYNQKVKGRTISIDKSKNTLYLQMNLSRAEDTAVYYCARWDYSHFDVWGQGTTVTVS S
2238	CH3 R170R CC - VL	artificial	EIVMTQSPATLSVSPGERATLTCRASSSVSYMHYQQKPGQAPRLLIYGTSNLVSQV ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSSYPLTFGCGTKVEIK
2239	CH3 15-E11 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYFTFTNYWMNWRQAPGQCLEWMGNIAYGKGT NYNQKFQGRVMTVDTSSSTAYMELSLRLSDDTAVYYCATRYFYVMDYWGQGTTLTVTS SGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQDISNYLNWYQQKPGK VPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCVQYAQFPLTFGC GTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGL EWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGSGQTVVTQEPSTLTVSPGGTIVLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGDKTLTVLGGGDKHTCPCPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTK NQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYK TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2240	CH3 15-E11 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYFTFTNYWMNWRQAPGQCLEWMGNIAYGKGT NYNQKFQGRVMTVDTSSSTAYMELSLRLSDDTAVYYCATRYFYVMDYWGQGTTLTVTS SGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQDISNYLNWYQQKPGK VPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCVQYAQFPLTFGC GTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWRQAPGKGL EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVYYCARAGN FGSSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGSGQTVVTQEPSTLTVSPGGTIVT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKTLTVLGGGDKHTCPCPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTK NQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYK TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2241	CH3 15-E11 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYFTFTNYWMNWRQAPGQCLEWMGNIAYGKGT NYNQKFQGRVMTVDTSSSTAYMELSLRLSDDTAVYYCATRYFYVMDYWGQGTTLTVTS SGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQDISNYLNWYQQKPGK VPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCVQYAQFPLTFGC GTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGL EWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVYYCVRNEN IGTSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGSGQTVVTQEPSTLTVSPGGTIVT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKTLTVLGGGDKHTCPCPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTK NQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ

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	Sequence		NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQYYSYPTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNRYA INWVRQAPGKGLWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQNNLKE DTAVYYCARAGNFGSSYISYWAYWGQGLTIVTVSSGGGGSGGGSGGGSGTQVTVTQEPS LTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAPGTARFSGS LSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTTCCPPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG GGSGGGSGGGSGDKHTTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQK SLSLSPGK
2247	CH3 G8A 6- B12 x I2K x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLWVGVIWITGGGTN YASSVKGRFTISRDNKNTVYLQNNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLVTVSSGGGGSGGGSGGGSDIVMTQSPDLSLAVSLGERATINCKSSQSLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQYYSYPTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNRYA MNWVRQAPGKGLWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQNNLKE DTAVYYCVRNENIGTSYISYWAYWGQGLTIVTVSSGGGGSGGGSGGGSGTQVTVTQEPS LTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAPGTARFSGS LSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTTCCPPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG GGSGGGSGGGSGDKHTTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQK SLSLSPGK
2248	CH3 G8A 6- B12 x I2L x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLWVGVIWITGGGTN YASSVKGRFTISRDNKNTVYLQNNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLVTVSSGGGGSGGGSGGGSDIVMTQSPDLSLAVSLGERATINCKSSQSLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQYYSYPTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNRYA MNWVRQAPGKGLWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQNNLKE DTAVYYCVRAGNFGSSYISYFAYWGQGLTIVTVSSGGGGSGGGSGGGSGTQVTVTQEPS LTVSPGGTIVTITCGSSTGAVTSGNYPNWIQKKPGQAPRGLIGGTKFLAPGTARFSGS LEGGKAALTLGSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKHTTCCPPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG GGSGGGSGGGSGDKHTTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQK SLSLSPGK
2249	CH3 G8A 6- B12 x I2M x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLWVGVIWITGGGTN YASSVKGRFTISRDNKNTVYLQNNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLVTVSSGGGGSGGGSGGGSDIVMTQSPDLSLAVSLGERATINCKSSQSLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQYYSYPTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNRYA MNWVRQAPGKGLWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQNNLKE DTAVYYCVRAGNFGTSYISYWAYWGQGLTIVTVSSGGGGSGGGSGGGSGTQVTVTQEPS LTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAPGTARFSGS LSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTTCCPPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG GGSGGGSGGGSGDKHTTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQK SLSLSPGK
2250	CH3 G8A 6- B12 x I2M2 x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLWVGVIWITGGGTN YASSVKGRFTISRDNKNTVYLQNNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLVTVSSGGGGSGGGSGGGSDIVMTQSPDLSLAVSLGERATINCKSSQSLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQYYSYPTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNRYA INWVRQAPGKGLWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQNNLKE DTAVYYCVRNANFGTSYISYFAYWGQGLTIVTVSSGGGGSGGGSGGGSGTQVTVTQEPS LTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAPGTARFSGS

			LLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAP ELLGGPVSFLFPPKPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLL YSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQK SLSLSPGK
2251	CH3 R170R CC x I2C x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTISIDKSKNTLYLQMNSLRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG PRLLIYGTSNLVSQVGPVGFSGSGSGTEFTLTISLQSGEDFAVYYCQQWSSYPLTFGCG TKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGL WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGTITVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPVSFLFPP KPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPVSFLFPPKPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PPVLDSDGSFLLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK
2252	CH3 R170R CC x I2E x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTISIDKSKNTLYLQMNSLRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG PRLLIYGTSNLVSQVGPVGFSGSGSGTEFTLTISLQSGEDFAVYYCQQWSSYPLTFGCG TKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGL WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAVYYCARAGNF GSSYISYWAYWGQGTITVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPVSFLFPP KPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPVSFLFPPKPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PPVLDSDGSFLLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK
2253	CH3 R170R CC x I2K x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTISIDKSKNTLYLQMNSLRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG PRLLIYGTSNLVSQVGPVGFSGSGSGTEFTLTISLQSGEDFAVYYCQQWSSYPLTFGCG TKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGL WVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDTAVYYCVRNENI GTSYISYWAYWGQGTITVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPVSFLFPP KPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPVSFLFPPKPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PPVLDSDGSFLLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK
2254	CH3 R170R CC x I2L x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTISIDKSKNTLYLQMNSLRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG PRLLIYGTSNLVSQVGPVGFSGSGSGTEFTLTISLQSGEDFAVYYCQQWSSYPLTFGCG TKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGL WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVYYCVRAGNF GSSYISYWAYWGQGTITVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGV QPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPVSFLFPP KPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQ GNVFSQSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPVSFLFPPKPKDTLMI SRT PEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PPVLDSDGSFLLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

			PPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2255	CH3 R170R CC x I2M x scFc - Full Sequence	artificial	EVQLLESGLLVQPGGSLRLSCAASGFTFSSYMMHWVRQTPGKCLEWWSKIDPDDYT NYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMMHWYQKPGQA PRLLIYGTSNLVSGVPARFSGSGSGTEFTLTISLQSEDFAVYYCQWSSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKME WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNF GTSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTITITC GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLGSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFPP KPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKN QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQ GNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2256	CH3 R170R CC x I2M2 x scFc - Full Sequence	artificial	EVQLLESGLLVQPGGSLRLSCAASGFTFSSYMMHWVRQTPGKCLEWWSKIDPDDYT NYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMMHWYQKPGQA PRLLIYGTSNLVSGVPARFSGSGSGTEFTLTISLQSEDFAVYYCQWSSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVREAPGKGLE WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVNRNANF GTSYISYFAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGGTITITC GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLGSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFPP KPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKN QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQ GNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2257	CL1 7-D7 CC - HCDR1	artificial	NYMH
2258	CL1 7-D7 CC - HCDR2	artificial	WINPTSGGANYAQKFQG
2259	CL1 7-D7 CC - HCDR3	artificial	ESHAIQEGIWFDY
2260	CL1 7-D7 CC - LCDR1	artificial	RASQSISNYLN
2261	CL1 7-D7 CC - LCDR2	artificial	DASSLQS
2262	CL1 7-D7 CC - LCDR3	artificial	QQSYSFPLT
2263	CL1 7-D7 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVCKASGYFTFTNYMMHWVRQAPGQCLEWMMWINPTSGGA NYAQKFQGRVTMTSDTSTAYMELSLRLSDDTAVYFCARESHAQEGIWFDYWGQGT LVTVSS
2264	CL1 7-D7 CC - VL	artificial	DIQMTQSPSSLSASVGDRTVTSRCSQSISNYLNWYQKPGKAPKLLIYDASSLQSGV PSRFGSGSGTDFTLTISLQPEDFATYYCQSYSFPLTFGCGTKVEIK
2265	CL1 7-D7 CC EI GQ - VL	artificial	BIQMTQSPSSLSASVGDRTVTSRCSQSISNYLNWYQKPGKAPKLLIYDASSLQSGV PSRFGSGSGTDFTLTISLQPEDFATYYCQSYSFPLTFGCGTKVEIK
2266	CL1 7-D7 CC x I2Cx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYFTFTNYMMHWVRQAPGQCLEWMMWINPTSGGA NYAQKFQGRVTMTSDTSTAYMELSLRLSDDTAVYFCARESHAQEGIWFDYWGQGT LVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVTSRCSQSISNYLNWYQ KPGKAPKLLIYDASSLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQSYSFPL LTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAP PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTVSPGG TVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGY STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSR EEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPE NNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2267	CL1 7-D7 CC x I2Ex scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYFTFTNYMMHWVRQAPGQCLEWMMWINPTSGGA NYAQKFQGRVTMTSDTSTAYMELSLRLSDDTAVYFCARESHAQEGIWFDYWGQGT LVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVTSRCSQSISNYLNWYQ KPGKAPKLLIYDASSLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQSYSFPL

			LTFCGCTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVYVC ARAGNFGSSYISYWAYWGQGLTTLTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLGSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2268	CL1 7-D7 CC x I2Kx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYFTFTNYYMHVVRQAPGQCLEWMGWINFTSGGA NYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYFCARESHAIQEGIFDYGWGGT LVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTISCRASQSIISNYLWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYCCQSYFSP LTFCGCTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVYVC VRNENIGTSYISYWAYWGQGLTTLTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLGSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2269	CL1 7-D7 CC x I2Lx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYFTFTNYYMHVVRQAPGQCLEWMGWINFTSGGA NYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYFCARESHAIQEGIFDYGWGGT LVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTISCRASQSIISNYLWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYCCQSYFSP LTFCGCTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYVC VRAGNFGTSYISYFAYWGQGLTTLTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLGSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2270	CL1 7-D7 CC x I2M2x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYFTFTNYYMHVVRQAPGQCLEWMGWINFTSGGA NYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYFCARESHAIQEGIFDYGWGGT LVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTISCRASQSIISNYLWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYCCQSYFSP LTFCGCTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYVC VRNANFGTSYISYFAYWGQGLTTLTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLGSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2271	CL1 7-D7 CC x I2Mx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYFTFTNYYMHVVRQAPGQCLEWMGWINFTSGGA NYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYFCARESHAIQEGIFDYGWGGT LVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTISCRASQSIISNYLWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYCCQSYFSP LTFCGCTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYVC VRAGNFGTSYISYWAYWGQGLTTLTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLGSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS

			VFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPG K
2272	CS PDL241.12.L H CC - HCDR1	artificial	SSWMN
2273	CS PDL241.12.L H CC - HCDR2	artificial	RIYPGDADAKYNKFKG
2274	CS PDL241.12.L H CC - HCDR3	artificial	STMIATGAMDY
2275	CS PDL241.12.L H CC - LCDR1	artificial	KASQDVSTAVA
2276	CS PDL241.12.L H CC - LCDR2	artificial	SASYRYT
2277	CS PDL241.12.L H CC - LCDR3	artificial	QQHYSTPPYT
2278	CS PDL241.12.L H CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYAFSSSSWMNWVRQAPGQCLEWIGRIYPGDADA KYNKFKGKATLTADKSTSTAYMELSSLSRSEDVAVYCARSTMIATGAMDYWGQGLTV TVSS
2279	CS PDL241.12.L H CC - VL	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITISLQPEDFATYYCQQHYSTPPYTFCGCGTKVEIKRGGGGSGG
2280	CS PDL241.12.L H CC x I2C x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITISLQPEDFATYYCQQHYSTPPYTFCGCGTKVEIKRGGGGSGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCKASGYAFSSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNKFKGKATLTADKSTSTAYMELSSLSRSEDVAVYCARSTMIATGAMD YWGQGLTVLTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRISKYNNYATYYADSVKDRFTISRDDSKNTAYLQNMNKLKTEDTAVYYC VRHNGFNGSYISYWAYWGQGLTVTVSSSGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGG TVTITCGSGTGAVTSGNYPNWQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLVGQVPDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPG K
2281	CS PDL241.12.L H CC x I2E x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITISLQPEDFATYYCQQHYSTPPYTFCGCGTKVEIKRGGGGSGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCKASGYAFSSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNKFKGKATLTADKSTSTAYMELSSLSRSEDVAVYCARSTMIATGAMD YWGQGLTVLTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRISKYNNYATYYADAVKDRFTISRDDSKNTVYLQNMNKLKTEDTAVYYC ARAGNFGSSYISYWAYWGQGLTVTVSSSGGGGSGGGGSGGGGSGTQVVTQEPSLTVSPGG TVTITCGSGTGAVTSGNYPNWQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLVGQVPDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPG K
2282	CS PDL241.12.L	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITISLQPEDFATYYCOHYSTPPYTFCGCGTKVEIKRGGGGSGG

	H CC x I2K x scFc - Full Sequence		GGSGGGGSQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDTAVYYCARSTMIATGAMD YWGQGTTLVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQA PGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMMNLKTEDTAVYYC VRNENIGTSYISYWAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTAVVTVQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYQ STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVD KSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYQSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPG K
2283	CS PDL241.12_L H CC x I2L x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGDFTLTITSSLPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDTAVYYCARSTMIATGAMD YWGQGTTLVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQA PGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMMNLKTEDTAVYYC VRAGNFGSSSYISYFAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTAVVTVQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLGSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYQ STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVD KSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYQSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPG K
2284	CS PDL241.12_L H CC x I2M x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGDFTLTITSSLPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDTAVYYCARSTMIATGAMD YWGQGTTLVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQA PGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMMNLKTEDTAVYYC VRAGNFGTSSYISYFAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTAVVTVQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYQ STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVD KSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYQSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPG K
2285	CS PDL241.12_L H CC x I2M2 x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGDFTLTITSSLPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDTAVYYCARSTMIATGAMD YWGQGTTLVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVREA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMMNLKTEDTAVYYC VRNANFGTSSYISYFAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTAVVTVQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYQ STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVD KSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYQSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPG K
2286	CL6 3D4- 01.G2 LH - HCDR1	artificial	GYMH
2287	CL6 3D4- 01.G2 LH - HCDR2	artificial	WINPNSGETNYAQKFQG
2288	CL6 3D4-	artificial	DALIVVAPVTRDYYYGMDV

	01.G2 LH - HCDR3		
2289	CL6 3D4- 01.G2 LH - LCDR1	artificial	RASQSVSSSYLA
2290	CL6 3D4- 01.G2 LH - LCDR2	artificial	GASSRAT
2291	CL6 3D4- 01.G2 LH - LCDR3	artificial	QQYGSSPLT
2292	CL6 3D4- 01.G2 LH - VH	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQCLEWMGWINPNSGET NYAQKFQGRVMTDRDTSISTAYMELSLRLSDDTAVYYCARDALIVVAVPTRDYYYGYM DVWGQGTITVTVSS
2293	CL6 3D4- 01.G2 LH - VL	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFCGCTKLEIK
2294	CL6 3D4- 01.G2 LH x I2Cx scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFCGCTKLEIKGGGSGGG GSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVMTDRDTSISTAYMELSLRLSDDTAVYYCARDALIVVAVPTR DYYYGYMDVWGQGTITVTVSSSGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKY AMNWVRQAPGKGLVAVARIIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSSGGGSGGGGSGGGGSGTAVVTQEP SLTVSPGGTITICGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSG SLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVTLVHQQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF LYSKLTVDKSRWQQGNVFSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSG GGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVTLVHQQDLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNNHYTQ KSLSLSPGK
2295	CL6 3D4- 01.G2 LH x I2Ex scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFCGCTKLEIKGGGSGGG GSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVMTDRDTSISTAYMELSLRLSDDTAVYYCARDALIVVAVPTR DYYYGYMDVWGQGTITVTVSSSGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKY AINWVRQAPGKGLVAVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLLQMNNLKT EDTAVYYCARAGNFGSSYISYWAYWGQGTITVTVSSSGGGSGGGGSGGGGSGTAVVTQEP SLTVSPGGTITICGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSG SLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVTLVHQQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF LYSKLTVDKSRWQQGNVFSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSG GGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVTLVHQQDLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNNHYTQ KSLSLSPGK
2296	CL6 3D4- 01.G2 LH x I2Kx scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFCGCTKLEIKGGGSGGG GSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVMTDRDTSISTAYMELSLRLSDDTAVYYCARDALIVVAVPTR DYYYGYMDVWGQGTITVTVSSSGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKY AMNWVRQAPGKGLVAVARIIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLLQMNNLKT EDTAVYYCVRNENIGTSYISYWAYWGQGTITVTVSSSGGGSGGGGSGGGGSGTAVVTQEP SLTVSPGGTITICGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSG SLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVTLVHQQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF LYSKLTVDKSRWQQGNVFSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSG GGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD DVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVTLVHQQDLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNNHYTQ KSLSLSPGK
2297	CL6 3D4- 01.G2 LH x I2Lx scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFCGCTKLEIKGGGSGGG GSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVMTDRDTSISTAYMELSLRLSDDTAVYYCARDALIVVAVPTR DYYYGYMDVWGQGTITVTVSSSGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKY AMNWVRQAPGKGLVAVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKT

			EDTAVYYCVRAGNFGSSSYISYFAYWGQGTTLTVSSGGGGSGGGGGSGGGGSQT VVTQEP SLTVSPGGT VTI TCGSSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKLAPGTPARFSG SLEGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF LYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGGGSGGGSG GGGGSGGGSGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQ KSLSLSPGK
2298	CL6 3D4- 01.G2 LH x I2M2x scFc - Full Sequence	artificial	EIVLTQSPGTLTSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGCGTKLEIKGGGGSGGG SGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTRDTSISTAYMELSLRLSDDTAVYYCARDALIVVAPVTR DYIYYGMDVWGQGT VTI TCGSSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKLAPGTPARFSG AINWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRNANFGTSYISYFAYWGQGTTLTVSSGGGGSGGGGGSGGGGSQT VVTQEP SLTVSPGGT VTI TCGSSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKLAPGTPARFSG SLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF LYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGGGSGGGSG GGGGSGGGSGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQ KSLSLSPGK
2299	CL6 3D4- 01.G2 LH x I2Mx scFc - Full Sequence	artificial	EIVLTQSPGTLTSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGCGTKLEIKGGGGSGGG SGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTRDTSISTAYMELSLRLSDDTAVYYCARDALIVVAPVTR DYIYYGMDVWGQGT VTI TCGSSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKLAPGTPARFSG AMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRAGNFGTSYISYWAYWGQGTTLTVSSGGGGSGGGGGSGGGGSQT VVTQEP SLTVSPGGT VTI TCGSSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKLAPGTPARFSG SLSGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF LYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGGGSGGGSG GGGGSGGGSGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQ KSLSLSPGK
2300	CL 10D8 CC - HCDR1	artificial	GYMH
2301	CL 10D8 CC - HCDR2	artificial	WINPNSGGTKYAQKFQG
2302	CL 10D8 CC - HCDR3	artificial	DRITVAGTYYYGMDV
2303	CL 10D8 CC - LCDR1	artificial	RASQGVNNWLA
2304	CL 10D8 CC - LCDR2	artificial	TASSLQS
2305	CL 10D8 CC - LCDR3	artificial	QQANSFPIT
2306	CL 10D8 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGT KYAQKFQGRVTMTRDTSISTAYMELSLRLSDDTAVYYCARDRITVAGTYYYGMDVWG QGTITVTVSS
2307	CL 10D8 CC - VL	artificial	DIQMTQSPSSVSASVGDRTVITCRASQGVNNWLAWYQQKPGKAPKLLIYTASSLQSGV PSRFGSGSGTDFTLTISRLEPEDFATYYCQQANSFPITFGCGTRLEIK
2308	CL 10D8 CC EI GQ - VL	artificial	EIQMTQSPSSVSASVGDRTVITCRASQGVNNWLAWYQQKPGKAPKLLIYTASSLQSGV PSRFGSGSGTDFTLTISRLEPEDFATYYCQQANSFPITFGCGTRLEIK
2309	CL 10D8 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGT KYAQKFQGRVTMTRDTSISTAYMELSLRLSDDTAVYYCARDRITVAGTYYYGMDVWG QGTITVTVSSGGGGSGGGGSDIQMTQSPSSVSASVGDRTVITCRASQGVNNWLA WYQQKPGKAPKLLIYTASSLQSGVPSRFGSGSGTDFTLTISRLEPEDFATYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWR QAPGKMEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGGSGGGGGSGGGGSQT VVTQEP SLTVSPGGT VTI TCGSSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKLAPGTPARFSG SLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEE

			QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2310	CL 10D8 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYMHVVRQAPGQCLEWMGWIPNSGGTKYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYYCARDRITVAGTYYYGMDVWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGVNNWLA WYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV RQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAV YYCARAGNFGSSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQTVVTQEPSTLTVS PGGTITITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGG KAAITLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVLFPPPKPDKTILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2311	CL 10D8 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYMHVVRQAPGQCLEWMGWIPNSGGTKYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYYCARDRITVAGTYYYGMDVWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGVNNWLA WYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMWV RQAPGKGLIEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDTAV YYCVNRNENIGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQTVVTQEPSTLTVS PGGTITITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGG KAAITLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVLFPPPKPDKTILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2312	CL 10D8 CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYMHVVRQAPGQCLEWMGWIPNSGGTKYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYYCARDRITVAGTYYYGMDVWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGVNNWLA WYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMWV RQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAV YYCVNRNENIGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQTVVTQEPSTLTVS PGGTITITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGG KAAITLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVLFPPPKPDKTILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2313	CL 10D8 CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYMHVVRQAPGQCLEWMGWIPNSGGTKYAQKFQGRVTMTDRDTSISTAYMELSLRLSDDTAVYYCARDRITVAGTYYYGMDVWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGVNNWLA WYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMWV RQAPGKGLIEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAV YYCVNRNENIGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQTVVTQEPSTLTVS PGGTITITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGT PARFSGSLSGG KAAITLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVLFPPPKPDKTILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK

			LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2314	CL 10D8 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVWRQAPGGQCLEWMGWPNPNSGGT KYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDRITVAGTYYYGMDVWG QGTITVTVSSGGGSGGGGSGGGGSDIQTQSPSSVSASVGDRTITCRASQGVNWL WYQQKPKGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINNW REAPGKGLWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNLLKTEDTAV YYCVRNANFGTSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSL SPGK
2315	DL 8-A7 CC - HCDR1	artificial	SYIYWS
2316	DL 8-A7 CC - HCDR2	artificial	YVYVSGTTNYPNLSLKS
2317	DL 8-A7 CC - HCDR3	artificial	IAVTGIFYFDY
2318	DL 8-A7 CC - LCDR1	artificial	RASQRVNNNYLA
2319	DL 8-A7 CC - LCDR2	artificial	GASSRAT
2320	DL 8-A7 CC - LCDR3	artificial	QQYDRSPLT
2321	DL 8-A7 CC - VH	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYVSGTTN YNPSLKSRTISVDTSKNQFSLKLSSTVAADTAVYYCASIATVGFYFDYWGQGTILVT SS
2322	DL 8-A7 CC - VL	artificial	EIVLTQSPGTLSTLSPGERVTLSCRASQRVNNNYLAWYQQRPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGCGTKLEIK
2323	DL 8-A7 CC x I2C x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYVSGTTN YNPSLKSRTISVDTSKNQFSLKLSSTVAADTAVYYCASIATVGFYFDYWGQGTILVT SSGGGSGGGGSGGGGSEIVLTQSPGTLSTLSPGERVTLSCRASQRVNNNYLAWYQQR GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGGSGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2324	DL 8-A7 CC x I2E x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYVSGTTN YNPSLKSRTISVDTSKNQFSLKLSSTVAADTAVYYCASIATVGFYFDYWGQGTILVT SSGGGSGGGGSGGGGSEIVLTQSPGTLSTLSPGERVTLSCRASQRVNNNYLAWYQQR GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINNWRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTEDTAVYYCARA GNFGSSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTITCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2325	DL 8-A7 CC x I2K x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYVSGTTN YNPSLKSRTISVDTSKNQFSLKLSSTVAADTAVYYCASIATVGFYFDYWGQGTILVT SSGGGSGGGGSGGGGSEIVLTQSPGTLSTLSPGERVTLSCRASQRVNNNYLAWYQQR GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK

			GLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMMNLKTEDTAVYYCVRN ENIGTSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCWLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS RCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2326	DL 8-A7 CC x I2L x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTISVDTSKNQFSLKLSSTVTAADTAVYYCASIATVGFYFDYWGQGTILVT SSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERVTLSCRASQVRNNNYLAWYQQR GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYDRSPLTF GCGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMMNLKTEDTAVYYCVRN GNFGSSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCWLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS RCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2327	DL 8-A7 CC x I2M x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTISVDTSKNQFSLKLSSTVTAADTAVYYCASIATVGFYFDYWGQGTILVT SSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERVTLSCRASQVRNNNYLAWYQQR GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYDRSPLTF GCGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMMNLKTEDTAVYYCVRN GNFGTSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCWLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS RCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2328	DL 8-A7 CC x I2M x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTISVDTSKNQFSLKLSSTVTAADTAVYYCASIATVGFYFDYWGQGTILVT SSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERVTLSCRASQVRNNNYLAWYQQR GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYDRSPLTF GCGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMMNLKTEDTAVYYCVRN ANFGTSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCWLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS RCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2329	EGFRvIII CC - HCDR1	artificial	NYGMH
2330	EGFRvIII CC - HCDR2	artificial	VIWYDGSCKYADSVRG
2331	EGFRvIII CC - HCDR3	artificial	DGYDILTGPNRDFDY
2332	EGFRvIII CC - LCDR1	artificial	RSSQSLVHSDGNTYLS
2333	EGFRvIII CC - LCDR2	artificial	RISRRFS
2334	EGFRvIII CC - LCDR3	artificial	MQSTHVPRT
2335	EGFRvIII CC - VH	artificial	QVQLVESGGGVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMMNSLRAEDTAVYYCARDGYDILTGPNRDFDYWGQ

			GTLTVVSS
2336	EGFRvIII CC - VL	artificial	DTVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPRLLIYRISR RFSGVDPDRFSGSGAGTDFTLTISRVEAEDVGYYCMQSTHVPRTFGCGTKVEIK
2337	EGFRvIII CC x I2C - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLTVVSSGGGGSGGGSGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFRSGVDPDRFSGSGAGTDFTLTISRVEAEDVGYYC MQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGSGTAVTQEPS LTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LLGGKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGSGTKLTVL
2338	EGFRvIII CC x I2E - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLTVVSSGGGGSGGGSGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFRSGVDPDRFSGSGAGTDFTLTISRVEAEDVGYYC MQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA INWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTE DTAVYYCARAGNFGSSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGSGTAVTQEPS LTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LSGGKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGSGTKLTVL
2339	EGFRvIII CC x I2K - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLTVVSSGGGGSGGGSGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFRSGVDPDRFSGSGAGTDFTLTISRVEAEDVGYYC MQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTE DTAVYYCVRNENIGTSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGSGTAVTQEPS LTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LSGGKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGSGTKLTVL
2340	EGFRvIII CC x I2L - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLTVVSSGGGGSGGGSGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFRSGVDPDRFSGSGAGTDFTLTISRVEAEDVGYYC MQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTE DTAVYYCVRAGNFGSSYISYFAYWGQGTTLTVTVSSGGGGSGGGSGGGSGTAVTQEPS LTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LEGGKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGSGTKLTVL
2341	EGFRvIII CC x I2M - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLTVVSSGGGGSGGGSGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFRSGVDPDRFSGSGAGTDFTLTISRVEAEDVGYYC MQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTE DTAVYYCVRAGNFGTSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGSGTAVTQEPS LTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LSGGKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGSGTKLTVL
2342	EGFRvIII CC x I2M2 - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLTVVSSGGGGSGGGSGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFRSGVDPDRFSGSGAGTDFTLTISRVEAEDVGYYC MQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA INWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRNANFGTSYISYFAYWGQGTTLTVTVSSGGGGSGGGSGGGSGTAVTQEPS LTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LLGGKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGSGTKLTVL
2343	FL 7-A8 CC - HCDR1	artificial	NARMGV
2344	FL 7-A8 CC - HCDR2	artificial	HIFSNDEKSYSTSLKN
2345	FL 7-A8 CC - HCDR3	artificial	IVGYGSGWYGFDDY
2346	FL 7-A8 CC - LCDR1	artificial	RASQGIKNDLG
2347	FL 7-A8 CC - LCDR2	artificial	AASTLQS
2348	FL 7-A8 CC - LCDR3	artificial	LQHNYSYPLT
2349	FL 7-A8 CC - VH	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKSSKTQVVLMTNVPDVTATYYCARIVGYGSGWYGFDDYWGQ GTLTVVSS
2350	FL 7-A8 CC - VL	artificial	DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQQKPGKAPKRLIYAASTLQSGV PSRFGSGSGTEFTLTISLQPEDFATYYCLQHNYSYPLTFCGCTKVEIK
2351	FL 7-A8 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGRVITTCRASQGIKNDLGWYQQKPGKAPKRLIYAASTLQSGV PSRFGSGSGTEFTLTISLQPEDFATYYCLQHNYSYPLTFCGCTKVEIK

2352	FL 7-A8 CC x I2Cx scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLVTVSSGGGSGGGGSGGGGSDIQTQSPSSLASVGDVDTITCRASQGIKRLNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNKLKTEDTAVY YCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSGTQVTVQEPSTLTVSP GGTVITLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKG AALTLSGVQPEDEAEYYCVLWYSNRWVFGGKLTVLGGGDKHTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGSGGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2353	FL 7-A8 CC x I2Ex scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLVTVSSGGGSGGGGSGGGGSDIQTQSPSSLASVGDVDTITCRASQGIKRLNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAVY YCARAGNFGSSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSGTQVTVQEPSTLTVSP GGTVITLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKG AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGSGGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2354	FL 7-A8 CC x I2Ex scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLVTVSSGGGSGGGGSGGGGSDIQTQSPSSLASVGDVDTITCRASQGIKRLNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNVR QAPGKGLEWVARIRSKYNNYATYYAAEAVKGRFTISRDDSKNTVYLQMNKLKTEDTAVY YCVRNENIGTSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSGTQVTVQEPSTLTVSP GGTVITLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKG AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGSGGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2355	FL 7-A8 CC x I2Lx scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLVTVSSGGGSGGGGSGGGGSDIQTQSPSSLASVGDVDTITCRASQGIKRLNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNVR QAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVY YCVRAGNFGSSYISYFAYWGQGTLVTVSSGGGSGGGGSGGGGSGTQVTVQEPSTLTVSP GGTVITLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLEGKG AALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGSGGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2356	FL 7-A8 CC x I2M2x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLVTVSSGGGSGGGGSGGGGSDIQTQSPSSLASVGDVDTITCRASQGIKRLNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR

			EAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVNRNANFGTYSIYSYFAYWGQGLTVTVSSGGGGSGGGSGGGGSQTVVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCCPPCAPPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLSDSGSFYLSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGDKTHTCCPPCAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLSDSGSFYLSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLS PGK
2357	FL 7-A8 CC x I2Mx scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTTLTCTLSGFSLNNARMGVSRIQPPGKCLEWLAHIFSNDE KSYSTSLKRLNLTISKDSSKTQVVLTMNVDPVDTATYYCARIVGYGSGWYGFDFYWGQ GTLVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDVRVITCRASQGI RNDLWG YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLT ISSLQPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGTFNKYAMNWR QAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVY YCVRAGNFGTYSIYSWAYWGQGLTVTVSSGGGGSGGGSGGGGSQTVVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCCPPCAPPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLSDSGSFYLSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGGSGG GGSGGGGSGDKTHTCCPPCAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLSDSGSFYLSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLS PGK
2358	MA 10-B5 CC - HCDR1	artificial	NAWMS
2359	MA 10-B5 CC - HCDR2	artificial	RIRRSRYGGTTDYAAPVKG
2360	MA 10-B5 CC - HCDR3	artificial	PSYSGSYNNYFSVMDV
2361	MA 10-B5 CC - LCDR1	artificial	RTSQSISSYLN
2362	MA 10-B5 CC - LCDR2	artificial	AASSLQG
2363	MA 10-B5 CC - LCDR3	artificial	QQTYSMPFT
2364	MA 10-B5 CC - VH	artificial	EVQLVSGGGGLVQPGGSLRLSCAASGTFFSNAWMSWVRQAPGKCLEWVGRIRRSRYGG TDDYAAPVKGRFTISRDDSKNTLFLQMNLSKTEDTAVYYCTTPSYSGSYNNYFSVMDV WGQGTITVTVSS
2365	MA 10-B5 CC - VL	artificial	DIQMTQSPSSLSASVGDVRVITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGV PSRFSGSGSGTDFTLT ISSLQPEDFATYYCQQTYSMPFTFGCGTKVEIK
2366	MA 10-B5 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDVRVITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGV PSRFSGSGSGTDFTLT ISSLQPEDFATYYCQQTYSMPFTFGCGTKVEIK
2367	MA 10-B5 CC x I2C x scFc - Full Sequence	artificial	EVQLVSGGGGLVQPGGSLRLSCAASGTFFSNAWMSWVRQAPGKCLEWVGRIRRSRYGG TDDYAAPVKGRFTISRDDSKNTLFLQMNLSKTEDTAVYYCTTPSYSGSYNNYFSVMDV WGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDVRVITCRTSQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLT ISSLQPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGTFNKYAMN WVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSQTVVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGDKTHTCCPPCAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLSDSGSFYLS KLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGDKTHTCCPPCAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLSDSGSFYLSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSL SLSPGK
2368	MA 10-B5 CC x I2E x scFc - Full Sequence	artificial	EVQLVSGGGGLVQPGGSLRLSCAASGTFFSNAWMSWVRQAPGKCLEWVGRIRRSRYGG TDDYAAPVKGRFTISRDDSKNTLFLQMNLSKTEDTAVYYCTTPSYSGSYNNYFSVMDV WGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDVRVITCRTSQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLT ISSLQPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGTFNKYAIN WVRQAPGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDT AVYYCARAGNFGSSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSQTVVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCCPPCAPPEL

			LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGG SGGGSGGGSGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSL SLSPGK
2369	MA 10-B5 CC x I2K x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRI RSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNNYFVMDV WGQGT TTVTSVSGGGSGGGSGGGSGGGSDI QMTQSPSSLSASVGDRTITCRTSQSISY LNWYQQKPGRAPKLLIF AASSLQGGVPSRFSGSGSGTDFTLT ISSLPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGSGEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTLVYLMNNLKTEDT AVYYCVRNENIGTSYISYWAYWGQGT LTVTSVSGGGSGGGSGGGSGGGSGT VVTQEPSLT VSPGGT VTI TCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSL GGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGG SGGGSGGGSGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSL SLSPGK
2370	MA 10-B5 CC x I2L x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRI RSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNNYFVMDV WGQGT TTVTSVSGGGSGGGSGGGSGGGSDI QMTQSPSSLSASVGDRTITCRTSQSISY LNWYQQKPGRAPKLLIF AASSLQGGVPSRFSGSGSGTDFTLT ISSLPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGSGEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLVYLMNNLKTEDT AVYYCVRAGNFGSSYISYFAYWGQGT LTVTSVSGGGSGGGSGGGSGGGSGT VVTQEPSLT VSPGGT VTI TCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSL GGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGG SGGGSGGGSGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSL SLSPGK
2371	MA 10-B5 CC x I2M x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRI RSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNNYFVMDV WGQGT TTVTSVSGGGSGGGSGGGSGGGSDI QMTQSPSSLSASVGDRTITCRTSQSISY LNWYQQKPGRAPKLLIF AASSLQGGVPSRFSGSGSGTDFTLT ISSLPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGSGEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLVYLMNNLKTEDT AVYYCVRAGNFGTSYISYWAYWGQGT LTVTSVSGGGSGGGSGGGSGGGSGT VVTQEPSLT VSPGGT VTI TCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSL GGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGG SGGGSGGGSGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSL SLSPGK
2372	MA 10-B5 CC x I2M2 x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRI RSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNNYFVMDV WGQGT TTVTSVSGGGSGGGSGGGSGGGSDI QMTQSPSSLSASVGDRTITCRTSQSISY LNWYQQKPGRAPKLLIF AASSLQGGVPSRFSGSGSGTDFTLT ISSLPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGSGEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAIN WVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRNANFGTSYISYFAYWGQGT LTVTSVSGGGSGGGSGGGSGGGSGT VVTQEPSLT VSPGGT VTI LTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGT PARFSGSL GGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGG SGGGSGGGSGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDV

			HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2373	MA A103 CC x I2C x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYNPALKSRITISKDTSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSTSSLSASLGDRVTISCSASQGIHNNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSNTAYLQMMNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQTLVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSKTHTCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2374	MA A103 CC x I2E x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYNPALKSRITISKDTSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSTSSLSASLGDRVTISCSASQGIHNNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTAYLQMMNLKTEDTAVYYC ARAGNFGSSYISYWAYWGQTLVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCTPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSKTHTCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2375	MA A103 CC x I2K x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYNPALKSRITISKDTSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSTSSLSASLGDRVTISCSASQGIHNNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQA PGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSNTAYLQMMNLKTEDTAVYYC VRNENIGTSYISYWAYWGQTLVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCTPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSKTHTCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2376	MA A103 CC x I2L x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYNPALKSRITISKDTSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSTSSLSASLGDRVTISCSASQGIHNNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQA PGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSNTAYLQMMNLKTEDTAVYYC VRAGNFGSSYISYFAYWGQTLVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLAPGTARFSGSLGGKAA LTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCTPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSKTHTCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2377	MA A103 CC	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD

	x I2M x scFc - Full Sequence		KYYNPALKSRLTISKDTSNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWGAGT TVTVSSGGGGSGGGGGSGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGTFNKYAMNWVRQA PGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYVC VRAGNFGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPG K
2378	MA A103 CC x I2M2 x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNDD KYYNPALKSRLTISKDTSNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWGAGT TVTVSSGGGGSGGGGGSGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGTFNKYAINWVREA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYVC VRANFGTSYISYFAYWGQGLTVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTVSPGG TVTTLTCSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPG K
2379	MART A103 CC - HCDR1	artificial	TSGMNVG
2380	MART A103 CC - HCDR2	artificial	HIWNDDKYYNPALKS
2381	MART A103 CC - HCDR3	artificial	SYFGDYVWYFDV
2382	MART A103 CC - LCDR1	artificial	SASQGIHNYLN
2383	MART A103 CC - LCDR2	artificial	YTSSLHS
2384	MART A103 CC - LCDR3	artificial	QQYSKLPRT
2385	MART A103 CC - VH	artificial	QVTLKESGPGILQPSQTLSTCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNDD KYYNPALKSRLTISKDTSNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWGAGT TVTVSS
2386	MART A103 CC - VL	artificial	DIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQKPDGTVKLLIYYTSSLHSGV PSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLPRTFGCGTKLEIK
2387	MART A103 CC EI GQ - VL	artificial	EIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQKPDGTVKLLIYYTSSLHSGV PSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLPRTFGCGTKLEIK
2388	MS 15-B12 CC - HCDR1	artificial	SSSYFWG
2389	MS 15-B12 CC - HCDR2	artificial	NIYYSGSSNYPNLSKS
2390	MS 15-B12 CC - HCDR3	artificial	LPRGDRDAFDI
2391	MS 15-B12 CC - LCDR1	artificial	RASQGISNYLA
2392	MS 15-B12 CC - LCDR2	artificial	AASTLQS
2393	MS 15-B12 CC - LCDR3	artificial	QQSYSTPFT
2394	MS 15-B12 CC - VH	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYFWGWIRQPPGKCLEWIGNIYYSGS SNYPNLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARLPRGDRDAFDIWDGQGT MTVSS
2395	MS 15-B12 CC - VL	artificial	DIVMTQSPSSLSASVGRVITITCRASQGISNYLAWYQKPGKVPKLLIYAASTLQSGV PSRFSGSGSGTDFTLTITSLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
2396	MS 15-B12 CC EI GQ - VL	artificial	EIVMTQSPSSLSASVGRVITITCRASQGISNYLAWYQKPGKVPKLLIYAASTLQSGV PSRFSGSGSGTDFTLTITSLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
2397	MS 5-F11 -	artificial	DYYMT

	HCDR1		
2398	MS 5-F11 - HCDR2	artificial	YISSSGSTIYYADSVKG
2399	MS 5-F11 - HCDR3	artificial	DRNSHFDY
2400	MS 5-F11 - LCDR1	artificial	RASQGINTWLA
2401	MS 5-F11 - LCDR2	artificial	GASGLQS
2402	MS 5-F11 - LCDR3	artificial	QQAKSFPRT
2403	MS 5-F11 - VH	artificial	QVQLVESGGGLVLPKGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISRDNAKNSLFLQMNLSRAEDTAVYYCARDNRNSHFDYWGQGLTVTVSS
2404	MS 5-F11 - VL	artificial	DIQMTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQAKSFPRTFGQGTKEIK
2405	MS 5-F11 EI GQ - VL	artificial	EIQMTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQAKSFPRTFGQGTKEIK
2406	MS R4L CC - HCDR1	artificial	GYIYH
2407	MS R4L CC - HCDR2	artificial	WINPNSGGTNYAQKFQG
2408	MS R4L CC - HCDR3	artificial	VEAVAGREYYYFSGMDV
2409	MS R4L CC - LCDR1	artificial	SGEKLGDKYVY
2410	MS R4L CC - LCDR2	artificial	QSTKRPS
2411	MS R4L CC - LCDR3	artificial	QAYHASTAV
2412	MS R4L CC - VH	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYIYHWVRQAPGQCLEWGMWINPNSGGTNYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYYFSGMDVMWGQGTITVTVSS
2413	MS R4L CC - VL	artificial	SYELTQPPSVSVSPGQTASITCSGEKLGDKYVYVWYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVL
2414	MS 15-B12 CC x I2C x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYFWGWIQPPGKCLEWIGNIYYSGSNSYNPPLSKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWGQGTMTVTVSSGGGSGGGGSGGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCVRHGNFNGSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGT VTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDK SRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGK
2415	MS 15-B12 CC x I2E x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYFWGWIQPPGKCLEWIGNIYYSGSNSYNPPLSKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWGQGTMTVTVSSGGGSGGGGSGGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVYYCARAGNFGSSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGK
2416	MS 15-B12 CC x I2K x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYFWGWIQPPGKCLEWIGNIYYSGSNSYNPPLSKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWGQGTMTVTVSSGGGSGGGGSGGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVYYCVRNENIGTSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGT

			VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTAPARFSGSLSGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLGGPSV FLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2417	MS 15-B12 CC x I2L x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYFWGWIROPFGKCLEWIGNIYYSGS SNYNPSLKSRTISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWGQGTMT VTVSSGGGGSGGGSGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQGSYSTPF TFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGTLTVTSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGG GGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2418	MS 15-B12 CC x I2M x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYFWGWIROPFGKCLEWIGNIYYSGS SNYNPSLKSRTISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWGQGTMT VTVSSGGGGSGGGSGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQGSYSTPF TFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGTLTVTSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGG GGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2419	MS 15-B12 CC x I2M2 x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYFWGWIROPFGKCLEWIGNIYYSGS SNYNPSLKSRTISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWGQGTMT VTVSSGGGGSGGGSGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQGSYSTPF TFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGTLTVTSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGG GGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2420	MS 5-F11 x I2Cx scFc - Full Sequence	artificial	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKLEWLSYISSSGSTI YYADSVKGRFTISRDNKNSFLQMNSLRAEDTAVYYCARDNRNSHFDYWGQGTLTIVS SGGGSGGGSGGGSGGGSDIQTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAQSFRTFGQ GKTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGL EWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGTLTVTSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGG CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTAPARFSGSLGGKAALTLSSG VQPEDEAEYYCVLWYSNRWVFGGGLKTLTVLGGGGDKTHTCPCPAPELLGGPSVFLFPP KPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKHTCPCPAPELLGGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT

			TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2421	MS 5-F11 x I2Ex scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVTS SGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAISFPRTFGQ GKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGN FGSSYISYWAYWGQGLTLTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTIVIT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTK NQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2422	MS 5-F11 x I2Kx scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVTS SGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAISFPRTFGQ GKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYAAVAKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVNRNEN IGTSYISYWAYWGQGLTLTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTIVIT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTK NQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2423	MS 5-F11 x I2Lx scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVTS SGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAISFPRTFGQ GKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVNRNEN FGSSYISYFAYWGQGLTLTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTIVIT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTK NQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2424	MS 5-F11 x I2M2x scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVTS SGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAISFPRTFGQ GKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVNRNEN FGTSYISYFAYWGQGLTLTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTIVIT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTK NQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2425	MS 5-F11 x I2Mx scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVTS SGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAISFPRTFGQ GKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVNRNEN FGTSYISYWAYWGQGLTLTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTIVIT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSG

			VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2426	MS R4L CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYIHVVRQAPGQCLEWMGWIPNSGGTNYAQKFQGRVTMTSDTSTISAYMELSLRSDDTAVYYCARVEAVAGREYYFSGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYQYQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSGGTITVTCGSSGTAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLTSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2427	MS R4L CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYIHVVRQAPGQCLEWMGWIPNSGGTNYAQKFQGRVTMTSDTSTISAYMELSLRSDDTAVYYCARVEAVAGREYYFSGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYQYQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCARAGNFGSSYISYWAYWGQGLVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSGGTITVTCGSSGTAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLTSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2428	MS R4L CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYIHVVRQAPGQCLEWMGWIPNSGGTNYAQKFQGRVTMTSDTSTISAYMELSLRSDDTAVYYCARVEAVAGREYYFSGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYQYQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRNENIGTSYISYWAYWGQGLVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSGGTITVTCGSSGTAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLTSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2429	MS R4L CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYIHVVRQAPGQCLEWMGWIPNSGGTNYAQKFQGRVTMTSDTSTISAYMELSLRSDDTAVYYCARVEAVAGREYYFSGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYQYQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLGGGGSEVQLVSGGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGLVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSGGTITVTCGSSGTAVTSGNYFNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLTSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

			DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGK
2430	MS R4L CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYYIHWRQAPGQCLEWGMWINFNSGGTNYAQKFQGRVTMTSDTSISTAYMELSLRSDDTAVYYCARVEAVAGREYIYFSGMDVWGGQTTTVTVSSGGGGSGGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYWYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGTLLTVTVSSGGGGSGGGGGSGGGGSQTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGKGGGGSGGGSDKTHTCPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGK
2431	MS R4L CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYYIHWRQAPGQCLEWGMWINFNSGGTNYAQKFQGRVTMTSDTSISTAYMELSLRSDDTAVYYCARVEAVAGREYIYFSGMDVWGGQTTTVTVTVSSGGGGSGGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYWYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWGQGTLLTVTVSSGGGGSGGGGGSGGGGSQTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGKGGGGSGGGSDKTHTCPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGK
2432	MU 8-B7 CC - HCDR1	artificial	GYYSWS
2433	MU 8-B7 CC - HCDR2	artificial	DIDASGSTKYNPISLKS
2434	MU 8-B7 CC - HCDR3	artificial	KKYSTVWSYFDN
2435	MU 8-B7 CC - LCDR1	artificial	SGDKLGDKYAS
2436	MU 8-B7 CC - LCDR2	artificial	QDRKRPS
2437	MU 8-B7 CC - LCDR3	artificial	QAWGSSTAV
2438	MU 8-B7 CC - VH	artificial	QVQLQQWAGLLKPSSETLSLTCVAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTKYNPSLKSRTISLDTSKNQFSLKLSNVTAAATAVYFCARKKYSTVWSYFDNWGQGTILVTVSS
2439	MU 8-B7 CC - VL	artificial	SYELTQPSSSVPPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVFGCGTKLTVL
2440	MU 8-B7 CC x I2Cx scFc - Full Sequence	artificial	QVQLQQWAGLLKPSSETLSLTCVAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTKYNPSLKSRTISLDTSKNQFSLKLSNVTAAATAVYFCARKKYSTVWSYFDNWGQGTILVTVSSGGGGSGGGGGSGGGSSYELTQPPSVSVPPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVFGCGTKLTVLSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVTVSSGGGGSGGGGGSGGGGSQTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGKGGGGSGGGSDKTHTCPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGK
2441	MU 8-B7 CC x I2Ex scFc - Full	artificial	QVQLQQWAGLLKPSSETLSLTCVAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTKYNPSLKSRTISLDTSKNQFSLKLSNVTAAATAVYFCARKKYSTVWSYFDNWGQGTILVTVSSGGGGSGGGGGSGGGSSYELTQPPSVSVPPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVFGCGTKLTVLSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVTVSSGGGGSGGGGGSGGGGSQTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKLSLSLSPGK

	Sequence		GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSSTAVF GCGTKLTIVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTVYLQMNNLKTEDTAVYVCARA GNFGSSYSYWAYWGQGTILVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTIVLGGGDKTHTCCPPCAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYKSLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NMYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYKSLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2442	MU 8-B7 CC x I2Kx scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGTILV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSSTAVF GCGTKLTIVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSNTVYLQMNNLKTEDTAVYVCVRN ENIGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTIVLGGGDKTHTCCPPCAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYKSLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NMYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYKSLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2443	MU 8-B7 CC x I2Lx scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGTILV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSSTAVF GCGTKLTIVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTLYLQMNNLKTEDTAVYVCVRA GNFGSSYSYFAYWGQGTILVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLYYSNRWVFGSGTKLTIVLGGGDKTHTCCPPCAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYKSLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NMYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYKSLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2444	MU 8-B7 CC x I2M2x scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGTILV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSSTAVF GCGTKLTIVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTAYLQMNNLKTEDTAVYVCVRN ANFGTSYISYFAYWGQGTILVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTIVLGGGDKTHTCCPPCAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYKSLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NMYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYKSLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2445	MU 8-B7 CC x I2Mx scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGTILV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSSTAVF GCGTKLTIVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTLYLQMNNLKTEDTAVYVCVRA GNFGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSQTVVTQEPSTLTVSPGGTIVT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTIVLGGGDKTHTCCPPCAPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYKSLTVDKSR

[illegible]

			VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSLSGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2467	PM 76-B10x I2L - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDDYMYWVRQAPGKGLEWVAIISDGGYYT YYSDIIGKRFTIISRDNAKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMDYWGQGT VTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCKASQNVDTNVAWYQQ KPGQAPKSLIYSASYRSDVPSRFSGSASGTDFTLTISVQSEDFFATYYCQYDSDPY TFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPFLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSLSGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2468	PM 76-B10x I2M - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDDYMYWVRQAPGKGLEWVAIISDGGYYT YYSDIIGKRFTIISRDNAKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMDYWGQGT VTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCKASQNVDTNVAWYQQ KPGQAPKSLIYSASYRSDVPSRFSGSASGTDFTLTISVQSEDFFATYYCQYDSDPY TFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPFLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSLSGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2469	PM 76-B10x I2M2 - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDDYMYWVRQAPGKGLEWVAIISDGGYYT YYSDIIGKRFTIISRDNAKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMDYWGQGT VTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCKASQNVDTNVAWYQQ KPGQAPKSLIYSASYRSDVPSRFSGSASGTDFTLTISVQSEDFFATYYCQYDSDPY TFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPFLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSLSGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2470	PM 76- B10.11 CC x I2C x scFc - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDDYMYWVRQAPGKGLEWVAIISDGGYYT YYSDIIGKRFTIISRDNAKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMDYWGQGT VTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCKASQNVDTNVAWYQQ KPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFTLTISVQSEDFFATYYCQYDQQLI TFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNVRQAP GKGMWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RHGNGFNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPFLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSLSGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGDKTHTCPAPPELLGGPSV FLFPPPKPDTLMSIRTPVETCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGGSFFLYSKLTVDK SRWQQGNVFSCSVMHREALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGGS GGGSGDKTHTCPAPPELLGGPSVFLFPPPKPDTLMSIRTPVETCVVDVSHEDPEV KFNWYVDGVEVHNNAKTKPCEEQYGSYTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPPVLDSDGGSFFLYSKLTVDKSRWQQGNVFSCSVMHREALHNNHYTQKSLSLSPGK
2471	PM 76- B10.11 CC x I2E x scFc - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDDYMYWVRQAPGKGLEWVAIISDGGYYT YYSDIIGKRFTIISRDNAKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMDYWGQGT VTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCKASQNVDTNVAWYQQ KPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFTLTISVQSEDFFATYYCQYDQQLI TFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVLYLQMNNLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPFLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSLSGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPAPPELLGGPSV FLFPPPKPDTLMSIRTPVETCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGGSFFLYSKLTVDK SRWQQGNVFSCSVMHREALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGGS GGGSGDKTHTCPAPPELLGGPSVFLFPPPKPDTLMSIRTPVETCVVDVSHEDPEV KFNWYVDGVEVHNNAKTKPCEEQYGSYTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPPVLDSDGGSFFLYSKLTVDKSRWQQGNVFSCSVMHREALHNNHYTQKSLSLSPGK
2472	PM 76- B10.11 CC x I2K x scFc - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDDYMYWVRQAPGKGLEWVAIISDGGYYT YYSDIIGKRFTIISRDNAKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMDYWGQGT VTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCKASQNVDTNVAWYQQ KPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFTLTISVQSEDFFATYYCQYDQQLI TFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINVRQAP GKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVLYLQMNNLKTEDTAVYYCV RNIETGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPFLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSLSGGKAAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPAPPELLGGPSV FLFPPPKPDTLMSIRTPVETCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGGSFFLYSKLTVDK SRWQQGNVFSCSVMHREALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGGS GGGSGDKTHTCPAPPELLGGPSVFLFPPPKPDTLMSIRTPVETCVVDVSHEDPEV KFNWYVDGVEVHNNAKTKPCEEQYGSYTYRCVSVLTVLHQDWLNGKEYCKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPPVLDSDGGSFFLYSKLTVDKSRWQQGNVFSCSVMHREALHNNHYTQKSLSLSPGK

			KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIKSAKGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2473	PM 76- B10.11 CC x I2L x scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGESLRLSCAASGFTFSDDYMYWVRQAPGKCLEWVAIISDGGYYT YYSDIIKGRFTISRDNAKNSLYLQMNSLKAEDTAVYYCARGFLLRHGAMDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQNVDTNVAWYQQ KPGQAPKSLIYASAYVYWDVPSRFSGSASGTDFTLTISVQSEDFATYYCQQYDQQLI TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAP GKGMWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RAGNFGSSYISYFAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCCPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIKSAKGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2474	PM 76- B10.11 CC x I2M x scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGESLRLSCAASGFTFSDDYMYWVRQAPGKCLEWVAIISDGGYYT YYSDIIKGRFTISRDNAKNSLYLQMNSLKAEDTAVYYCARGFLLRHGAMDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQNVDTNVAWYQQ KPGQAPKSLIYASAYVYWDVPSRFSGSASGTDFTLTISVQSEDFATYYCQQYDQQLI TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAP GKGMWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCCPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIKSAKGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2475	PM 76- B10.11 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVESGGGLVLPKGESLRLSCAASGFTFSDDYMYWVRQAPGKCLEWVAIISDGGYYT YYSDIIKGRFTISRDNAKNSLYLQMNSLKAEDTAVYYCARGFLLRHGAMDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQNVDTNVAWYQQ KPGQAPKSLIYASAYVYWDVPSRFSGSASGTDFTLTISVQSEDFATYYCQQYDQQLI TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRAP GKGLEWVARIIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RANFGTSYISYFAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCCPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIKSAKGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2505	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTRDKSTSTVYMESSLTSEDYAVYYCARVHDYDRAMEYWGQGT TVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQKPK GKGPCLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLPEDIATYYCQYASYPPTF GCGTRLEIKSGGGGQVQLVQSGAEVKKPGASVKVCKASGYTFTSYGISWVRQAPGQ CLEWMGWISAYSIGNAIYAQKLQGRVTMTDRDSTSTAYMELRSLRSDDTAVYYCARPD YYGSGSYSDYWGQGTTLTVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTITSSLSQ EDFAVYYCQQYHWSWFLITFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKGLEWVARIIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGG QTVTVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAP GTTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGGKTTLTVLGGGGDKT HTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGKGGGGSGG GGGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIKSAKGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNNHYTQKLSLSLSPGK
2506	CD20 99-E5	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT

	CC x CD22 28-B7 N65S CC x I2E x scFc - Full Sequence		EYNQKFKGRVMTMRDKSTSTVYMESSSLTSEDVAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTSYGISSWVRQAPGQ CLEWMGWISAYSGNAIYAQKLQGRVMTMRDSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGLTTLTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSS EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVY LQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGLTTLTVSSGGGSGGGGSGGGGS QTVVTQEPSTLTVSPGGTITTCGSSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNNHYTQKSLSLSPGKGGGSGGGG SGGGGSGGGGSGGGGSGGGGSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHE ALHNNHYTQKSLSLSPGK
2507	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVMTMRDKSTSTVYMESSSLTSEDVAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTSYGISSWVRQAPGQ CLEWMGWISAYSGNAIYAQKLQGRVMTMRDSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGLTTLTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSS EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVY LQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGLTTLTVSSGGGSGGGGSGGGGS QTVVTQEPSTLTVSPGGTITTCGSSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNNHYTQKSLSLSPGKGGGSGGGG SGGGGSGGGGSGGGGSGGGGSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHE ALHNNHYTQKSLSLSPGK
2508	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVMTMRDKSTSTVYMESSSLTSEDVAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTSYGISSWVRQAPGQ CLEWMGWISAYSGNAIYAQKLQGRVMTMRDSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGLTTLTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSS EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLY LQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGLTTLTVSSGGGSGGGGSGGGGS QTVVTQEPSTLTVSPGGTITTCGSSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNNHYTQKSLSLSPGKGGGSGGGG SGGGGSGGGGSGGGGSGGGGSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHE ALHNNHYTQKSLSLSPGK
2509	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVMTMRDKSTSTVYMESSSLTSEDVAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVCKASGYTFTSYGISSWVRQAPGQ CLEWMGWISAYSGNAIYAQKLQGRVMTMRDSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGLTTLTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSS EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLY LQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGLTTLTVSSGGGSGGGGSGGGGS QTVVTQEPSTLTVSPGGTITTCGSSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKLAP

[illegible]

			SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMELSSLS EDTAVYYCARVHDYDRAMEYWGQGTTVTVSSGGGGSGGGSGGGGSDIQTQSPSSLS ASVGDRVTITCKASQDINKYIAWYQQKPGKGPCLLIYYTSTLQPGVPSRFSGSGGTD FTFTISSLQPEDIAITYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSNTVYLQMNMLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTTLVTVSSGGGGSG GGSGGGGSGTVVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGL IGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2513	CD22 28- B7N65S CC x I2K x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2K - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSNGA IYAQKLQGRVTMTDRDTSTSTAYMELRSLRSDDTAVYYCARDPDYSGSGSYSDYWGQGT LVTVSSGGGGSGGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSNTVYLQMNMLKTEDTAVYY CVRNENIGTSYISYWAYWGQGTTLVTVSSGGGGSGGGGGSGGGGSGTVVVTQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGSGGGGGSGGGGSKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVTLVLHQQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGG GGSGGGGGSGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVLHQQDLNKG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALH HYTQKSLSLSPGKGGGGSGGGGGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYTFT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMELSSLS EDTAVYYCARVHDYDRAMEYWGQGTTVTVSSGGGGSGGGGGSGGGGSDIQTQSPSSLS ASVGDRVTITCKASQDINKYIAWYQQKPGKGPCLLIYYTSTLQPGVPSRFSGSGGTD FTFTISSLQPEDIAITYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISR RDDSNTVYLQMNMLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTTLVTVSSGGGGSG GGSGGGGSGTVVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGL IGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2514	CD22 28- B7N65S CC x I2L x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2L - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSNGA IYAQKLQGRVTMTDRDTSTSTAYMELRSLRSDDTAVYYCARDPDYSGSGSYSDYWGQGT LVTVSSGGGGSGGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQ APGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTLYLQMNMLKTEDTAVYY CVRAGNFGSSYISYFAYWGQGTTLVTVSSGGGGSGGGGGSGGGGSGTVVVTQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWIQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKA ALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGSGGGGGSGGGGSKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVTLVLHQQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGG GGSGGGGGSGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVLHQQDLNKG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALH HYTQKSLSLSPGKGGGGSGGGGGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYTFT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMELSSLS EDTAVYYCARVHDYDRAMEYWGQGTTVTVSSGGGGSGGGGGSGGGGSDIQTQSPSSLS ASVGDRVTITCKASQDINKYIAWYQQKPGKGPCLLIYYTSTLQPGVPSRFSGSGGTD FTFTISSLQPEDIAITYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISR RDDSNTLYLQMNMLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGTTLVTVSSGGGGSG GGSGGGGSGTVVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWIQKPKGQAPRGL IGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLT VL
2515	CD22 28- B7N65S CC x I2M x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2M - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSNGA IYAQKLQGRVTMTDRDTSTSTAYMELRSLRSDDTAVYYCARDPDYSGSGSYSDYWGQGT LVTVSSGGGGSGGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQ APGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTLYLQMNMLKTEDTAVYY CVRAGNFGTSYISYWAYWGQGTTLVTVSSGGGGSGGGGGSGGGGSGTVVVTQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGSGGGGGSGGGGSKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVTLVLHQQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGG GGSGGGGGSGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVT

			CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFIYPSD IAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHN HYTQKSLSLSPGKGGGSGGGGSGGGGSGVQLVQSGAEVKKPGASVKVSCKASGYFTT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMESSSLTS EDTAVYYCARVHDYDRAEMEYWGQGTITVTVSSGGGSGGGGSGGGGSDIQTQSPSSLS ASVGDRTVITCKASQDINKYIAWYQQKPKGPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLPQEDATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVSGGGGLVQPG GSLKLSAASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTIS RDDSNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGTITVTVSSGGGSG GGGSGGGGSGTVVTQEPSTLTVSPGGTITTCGSSTGAVTSGNYPNWVQKPKGQAPRGL IGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2516	CD22 28- B7N65S CC x I2M2 x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2M2 - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYGISWVRQAPGQCLEWMMGISAYSNGA IYAQKLQGRVTMTDRDTSTAYMELSLRSDTAVYVCARDPDYVGGSGSYSDYWGQGT LVTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSGEDFAVYICQQYHWSW LLTFGCGTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSAASGFTFNKYAINWVRE APGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTAYLQMNNLKTEDTAVYY CVRNANFGTSYISYFAYWGQGTITVTVSSGGGSGGGGSGGGGSGTVVTQEPSTLTVSPG GTVTLTCSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLGGKA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGSGGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGG GGSGGGGSGGGGSGGGGSDKTHTCPPEPAPELLGGPSVFLFPPKPKDTLMIISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFIYPSD IAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHN HYTQKSLSLSPGKGGGSGGGGSGGGGSGVQLVQSGAEVKKPGASVKVSCKASGYFTT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMESSSLTS EDTAVYYCARVHDYDRAEMEYWGQGTITVTVSSGGGSGGGGSGGGGSDIQTQSPSSLS ASVGDRTVITCKASQDINKYIAWYQQKPKGPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLPQEDATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVSGGGGLVQPG GSLKLSAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWGQGTITVTVSSGGGSG GGGSGGGGSGTVVTQEPSTLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGL IGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2517	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Cx scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYASARYTGV PDRFTGSGSGTDFTLTISLQPEDFATYYCQGHYSTPPYTFGCGTKVEIKRGGGSGGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDATVYYCARSTMTIATGAMD YWGGQGTITVTVSSGGGSGVQLVQSGAEVKKPGASVKVSCKASGYFTFNHIIHWVRQA PGQCLEWMMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMESSSLRSEDATVYYCAR DGYRDTVDVLDYWGQGTITVTVSSGGGSGGGGSGGGGSDIQTQSPSSLSASVGDRTV ITCQASQDISNYLWYQQKPKGAPKLLIYYTSLRLHTGVPSPRFSGSGSGTDFTFTISSL EPEDATYYCQGGNTLPWTFGCGTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSA ASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTA YLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGGSGGGGSGGGG SQTAVTQEPSTLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLA PGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPEPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTTP VLDSGGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKGGGSGGG GGSGGGGSGGGGSGGGGSDKTHTCPPEPAPELLGGPSVFLFPPKPKDTLMIISRT PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FIYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSQVMH EALHNHYTQKSLSLSPGK
2518	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Ex scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYASARYTGV PDRFTGSGSGTDFTLTISLQPEDFATYYCQGHYSTPPYTFGCGTKVEIKRGGGSGGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDATVYYCARSTMTIATGAMD YWGGQGTITVTVSSGGGSGVQLVQSGAEVKKPGASVKVSCKASGYFTFNHIIHWVRQA PGQCLEWMMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMESSSLRSEDATVYYCAR DGYRDTVDVLDYWGQGTITVTVSSGGGSGGGGSGGGGSDIQTQSPSSLSASVGDRTV ITCQASQDISNYLWYQQKPKGAPKLLIYYTSLRLHTGVPSPRFSGSGSGTDFTFTISSL EPEDATYYCQGGNTLPWTFGCGTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSA ASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTA YLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTITVTVSSGGGSGGGGSGGGG SQTAVTQEPSTLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLA PGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDK THTCPPEPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK

			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGG GGSGGGSGGSGGSGGSGGSGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMH EALHNYHTQKSLSLSPGK
2519	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Kx scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGDFTLTISLQPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGSGG GGSGGGSGQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDYAVYYCARSTMIATGAMD YWGQGTLLVTVSSSGGGSGQVQLVQSGAEVKKPGASVKVSCASGYFTFNHIIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMELSSLRSEDYAVYYCAR DGYRDTDLVDYWGQGTLLVTVSSSGGGSGGSGGSGGSDIQMTQSPSSLSASVGDRTIT ITCQASQDISNYLWYQQKPGKAPKLLIYYTSSLRLHTGVPSPRFSGSGSGTDFFTISSL EPEDIATYYCQGGNTLPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSA ASGFTFNKYAMNWRQAPGKGLWVARIRSKYNNYATYYAEAVKGRFTISRDSKNTV YLQMNLLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTLLVTVSSGGGSGGSGGSGG SQTAVTQEPSTLTVSPGGTITITCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLA PGTARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGG GGSGGGSGGSGGSGGSGGSGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMH EALHNYHTQKSLSLSPGK
2520	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Lx scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGDFTLTISLQPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGSGG GGSGGGSGQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDYAVYYCARSTMIATGAMD YWGQGTLLVTVSSSGGGSGQVQLVQSGAEVKKPGASVKVSCASGYFTFNHIIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMELSSLRSEDYAVYYCAR DGYRDTDLVDYWGQGTLLVTVSSSGGGSGGSGGSGGSDIQMTQSPSSLSASVGDRTIT ITCQASQDISNYLWYQQKPGKAPKLLIYYTSSLRLHTGVPSPRFSGSGSGTDFFTISSL EPEDIATYYCQGGNTLPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSA ASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDSKNTL YLQMNLLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGTLLVTVSSGGGSGGSGGSGG SQTAVTQEPSTLTVSPGGTITITCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLA PGTARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGG GGSGGGSGGSGGSGGSGGSGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMH EALHNYHTQKSLSLSPGK
2521	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2M2x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGDFTLTISLQPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGSGG GGSGGGSGQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDYAVYYCARSTMIATGAMD YWGQGTLLVTVSSSGGGSGQVQLVQSGAEVKKPGASVKVSCASGYFTFNHIIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMELSSLRSEDYAVYYCAR DGYRDTDLVDYWGQGTLLVTVSSSGGGSGGSGGSGGSDIQMTQSPSSLSASVGDRTIT ITCQASQDISNYLWYQQKPGKAPKLLIYYTSSLRLHTGVPSPRFSGSGSGTDFFTISSL EPEDIATYYCQGGNTLPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSA ASGFTFNKYAINWVRAPGKGLWVARIRSKYNNYATYYADAVKDRFTISRDSKNTA YLQMNLLKTEDTAVYYCVRNANFGTSYISYFAYWGQGTLLVTVSSGGGSGGSGGSGG SQTAVTQEPSTLTVSPGGTITITCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLA PGTARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGG GGSGGGSGGSGGSGGSGGSGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMH EALHNYHTQKSLSLSPGK
2522	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC	artificial	DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGDFTLTISLQPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGSGG GGSGGGSGQVQLVQSGAEVKKPGASVKVSCASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDYAVYYCARSTMIATGAMD

	x I2Mx scFc - Full Sequence		YWGQGTTLVTVSSSSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTHNHIIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFGGRATMTSDTSTSTVYMELSLSRSEDATVYYCAR DGYRDTDLVDYWGQGTTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVT ITCQASQDISNYLNWYQQKPKGAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFITISL EPEDIATYYCQQGNTLPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSA ASGFTFNKYAMNWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDSKNTL YLQMNNLKTEDTAVYYCVIRAGNFGTSYISYWAYWGQGTTLVTVSSGGGGSGGGGSGGGG SQTAVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLA PGTPARESGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTT VLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGG GGSGGGSGGGSGGGSGGGSGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPYSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMH EALHNHYTQKSLSLSPGK
2523	FL 7-A8 CC xCD123 24- B4-f NK CC x I2C x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYSGWYGFEDYWGQ GTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVTITCRASQGIIRNDLW YQQKPKGAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSVWR QAPGKCLEWWSAVSGGGDKTLYADAVKGRFTISRDNKNTLFLQMNLSRAEDTAIYYC ARLRGFFYYGMDVWGQGTITVTVSSGGGGSGGGGSGGGSDIVLTQSPSLSPVTPGEPAS ISCRSSQSLLSHNKYNLYLDWYLQKPGQSPQLLIYLSNRRASGVPRFSGSGSGTDFTL KISRVEADVGVVYCMQALQTPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DSKNTATYLMNNLKTEDTAVYYCVIRHGNFGNSYISYWAYWGQGTTLVTVSSGGGGSGGG GSGGGGSGTAVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIG GTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL GGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENN YKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK GGGGSGGGSGGGSGGGSGGGSGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNV FCSCVMHEALHNHYTQKSLSLSPGK
2524	FL 7-A8 CC xCD123 24- B4-f NK CC x I2E x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYSGWYGFEDYWGQ GTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVTITCRASQGIIRNDLW YQQKPKGAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSVWR QAPGKCLEWWSAVSGGGDKTLYADAVKGRFTISRDNKNTLFLQMNLSRAEDTAIYYC ARLRGFFYYGMDVWGQGTITVTVSSGGGGSGGGGSGGGSDIVLTQSPSLSPVTPGEPAS ISCRSSQSLLSHNKYNLYLDWYLQKPGQSPQLLIYLSNRRASGVPRFSGSGSGTDFTL KISRVEADVGVVYCMQALQTPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAINWRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISR DSKNTVYLMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTTLVTVSSGGGGSGGG GSGGGGSGTAVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIG GTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL GGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENN YKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK GGGGSGGGSGGGSGGGSGGGSGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNV FCSCVMHEALHNHYTQKSLSLSPGK
2525	FL 7-A8 CC xCD123 24- B4-f NK CC x I2K x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYSGWYGFEDYWGQ GTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVTITCRASQGIIRNDLW YQQKPKGAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSVWR QAPGKCLEWWSAVSGGGDKTLYADAVKGRFTISRDNKNTLFLQMNLSRAEDTAIYYC ARLRGFFYYGMDVWGQGTITVTVSSGGGGSGGGGSGGGSDIVLTQSPSLSPVTPGEPAS ISCRSSQSLLSHNKYNLYLDWYLQKPGQSPQLLIYLSNRRASGVPRFSGSGSGTDFTL KISRVEADVGVVYCMQALQTPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAFAVKGRTISR DSKNTVYLMNNLKTEDTAVYYCVIRNENIGTSYISYWAYWGQGTTLVTVSSGGGGSGGG GSGGGGSGTAVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIG GTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL GGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENN YKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

[illegible]

[illegible]

			TCRASSSVSYMHVYQKPGQAPRLLIYGTSNLVSGVVPARFSGSGSGTEFTLTISLQSS EDFAVYYCQWSSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYL QMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSQ TVVTQEPSTLTVSPGGTVTITCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPG TPARFSGSLSGGKAALTLVSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPY PSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMEAL LNNHYTQKSLSLSPGK
2533	MS R4L CC x CH3 R170R CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHVVRQAPGQCLEWMGWIPNSGGT NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTTLTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLLESGLLVQPGGSLRLSCAASGFTFSSYWMHWV RQTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYY CARWDYSHFDVWGQGTTLTVSSGGGGSGGGSGGGGSEIVMTQSPATLSVSPGERATL TCRASSSVSYMHVYQKPGQAPRLLIYGTSNLVSGVVPARFSGSGSGTEFTLTISLQSS EDFAVYYCQWSSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYL QMNNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSQ TVVTQEPSTLTVSPGGTVTITCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPG TPARFSGSLSGGKAALTLVSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPY PSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMEAL LNNHYTQKSLSLSPGK
2534	MS R4L CC x CH3 R170R CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHVVRQAPGQCLEWMGWIPNSGGT NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTTLTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLLESGLLVQPGGSLRLSCAASGFTFSSYWMHWV RQTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYY CARWDYSHFDVWGQGTTLTVSSGGGGSGGGSGGGGSEIVMTQSPATLSVSPGERATL TCRASSSVSYMHVYQKPGQAPRLLIYGTSNLVSGVVPARFSGSGSGTEFTLTISLQSS EDFAVYYCQWSSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYL QMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGTTLTVSSGGGGSGGGGSGGGGSQ TVVTQEPSTLTVSPGGTVTITCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPG TPARFSGSLEGGKAALTLVSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPY PSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMEAL LNNHYTQKSLSLSPGK
2535	MS R4L CC x CH3 R170R CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHVVRQAPGQCLEWMGWIPNSGGT NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTTLTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLLESGLLVQPGGSLRLSCAASGFTFSSYWMHWV RQTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYY CARWDYSHFDVWGQGTTLTVSSGGGGSGGGSGGGGSEIVMTQSPATLSVSPGERATL TCRASSSVSYMHVYQKPGQAPRLLIYGTSNLVSGVVPARFSGSGSGTEFTLTISLQSS EDFAVYYCQWSSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYL QMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSQ TVVTQEPSTLTVSPGGTVTITCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPG TPARFSGSLSGGKAALTLVSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFPY PSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMEAL LNNHYTQKSLSLSPGK

			EVTCTVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2536	MS R4L CC x CH3 R170R CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQCLEWMGWINFNSGGTNYAQKFQGRVTMTSDTSISTAYMELSRSDDTAVYYCARVEAVAGREYIYFSGMDVWGGQTTVTVSSGGGGSGGGGGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYVYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSLRAEDTAVYYCARWDYSHFDVWGQTTVTVSSGGGGSGGGGGGGSEIVMTQSPATLSVSPGERATLTCCRASSSVSYMHWYQKPKGQAPRLLIYGTSLNVSGVPPARFSGSGSGTEFTLTISLQSEDFAVYYCQWSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINVWREAPGKGLWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWGQGLTVTVSSGGGGSGGGGGSGGGGSGTVVTQEPSTLTVSPGGTIVLTGSSSTGAVTSGNYPNWWQKPKGQAPRGLIGGTKFLAPGTPARFSGSLGKGKAAITLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2551	{G4Q}3 - Linker	artificial	GGGGQGGGGQGGGGQ
2552	Human CD3epsilon ECD	artificial	QDGNEMGGITQTTPYKVISISGTTVILTCPPQYPGSEILWQHNDKNIGGEDDDKNIGSDE DHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMD
2553	Human CD3epsilon ECD / pos. 1-27	artificial	QDGNEMGGITQTTPYKVISISGTTVILT
2554	I2C_HC_H109 A- HCDR1	artificial	KYAMN
2555	I2C_HC_H109 A - HCDR2	artificial	RIRSKYNNYATYYADSVKD
2556	I2C_HC_H109 A - HCDR3	artificial	AGNFGNSYISYWAY
2557	I2C_HC_H109 A - LCDR1	artificial	GSSTGAVTSGNYPN
2558	I2C_HC_H109 A - LCDR2	artificial	GTKFLAP
2559	I2C_HC_H109 A - LCDR3	artificial	VLWYSNRVV
2560	I2C_HC_H109 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRAGNFGNSYISYWAYWGQGLTVTVSS
2561	I2C_HC_H109 A - VL	artificial	QTVVTQEPSTLTVSPGGTIVLTGSSSTGAVTSGNYPNWWQKPKGQAPRGLIGGTKFLAPGTPARFSGSLGKGKAAITLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

Claims

1. A polypeptide or polypeptide construct comprising:
 - 5 a binding domain binding to an extracellular epitope of the human CD3 ϵ chain comprising or consisting of a VH region and a VL region, wherein
 - i) the VH region comprises:
 - a CDR-H1 sequence of X₁YAX₂N, where X₁ is K, V, S, G, R, T, or I; and X₂ is M or I;
 - 10 a CDR-H2 sequence of RIRSKYNNYATYYADX₁VKX₂, where X₁ is S or Q; and X₂ is D, G, K, S, or E; and
 - a CDR-H3 sequence of HX₁NFGNSYX₂SX₃X₄AY, where X₁ is G, R, or A; X₂ is I, L, V, or T; X₃ is Y, W or F; and X₄ is W, F or Y; and
 - ii) wherein the VL region comprises:
 - 15 a CDR-L1 sequence of X₁SSTGAVTX₂X₃X₄YX₅N, where X₁ is G, R, or A; X₂ is S or T; X₃ is G or S; X₄ is N or Y; and X₅ is P or A;
 - a CDR-L2 sequence of X₁TX₂X₃X₄X₅X₆; where X₁ is G or A; X₂ is K, D, or N; X₃ is F, M or K; X₄ is L or R; X₅ is A, P, or V; and X₆ is P or S; and
 - a CDR-L3 sequence of X₁LWYSNX₂WV, where X₁ is V, A, or T; and X₂ is R or L;
 - 20 and
 - iii) wherein one or more of CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one amino acid substitution or a combination thereof selected from X₂4V and X₂4F in CDR-H1; D15, and X₁16A in CDR-H2;
 - 25 H1, X₁2E, F4, and N6 in CDR-H3; and
 - X₁1L and W3 in CDR-L3.
2. The polypeptide or polypeptide construct of claim 1, wherein in addition to said one amino acid substitution or a combination thereof as defined in iii) X₂ is I in said CDR-H1 sequence; X₂ is G in said CDR-H2 sequence; X₁ is A, X₄ is F in said CDR-H3 sequence; and/or X₁ is A in said CDR-L3 sequence.
3. The polypeptide or polypeptide construct of claim 1 or 2, comprising combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine,
 - 35 ten, eleven, twelve or more amino acid substitutions.
4. The polypeptide or polypeptide construct of any one of claims 1 to 3, wherein:

- i) said one amino acid substitution is selected from:
 a. X₂4V or X₂4F in CDR-H1; H1A in CDR-H3; and
 b. X₁1L and W3Y in CDR-L3;
- ii) said combination of two or more amino acid substitutions are selected from X₁16A in CDR-H2 and N6S in CDR-H3; and X₁16A in CDR-H2 and N6T in CDR-H3;
- iii) said combination of three or more amino acid substitutions are selected from X₁16A in CDR-H2, H1A and N6S in CDR-H3; X₁16A in CDR-H2, H1A and N6T in CDR-H3; X₁16A in CDR-H2, H1N and N6T in CDR-H3;
- iv) said combination of four or more amino acid substitutions are selected from X₁16A in CDR-H2, H1A, N6S in CDR-H3, and W3Y in CDR-L3; D15E, X₁16A in CDR-H2, H1A, and N6T in CDR-H3; D15E, X₁16A in CDR-H2, H1A, and N6S in CDR-H3; X₁16A in CDR-H2, H1A, F4I and N6S in CDR-H3; or
- v) said combination of five or six amino acid substitutions are selected from X₁16A in CDR-H2, H1A, X₁2E, F4I, and N6T in CDR-H3; X₁16A in CDR-H2, H1N, X₁2E, F4I, and N6S in CDR-H3; D15E, X₁16A in CDR-H2, H1A, N6S in CDR-H3; and W3Y in CDR-L3; D15E, X₁16A in CDR-H2, H1N, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, H1A, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, X₁2E, F4I and N6T in CDR-H3.
5. A polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region, wherein
- i) the VH region comprises the sequence of EVX₁LX₂ESGGGLX₃QPX₄GSLKLSCAASGFTFNX₅YAX₆NWVRQAPGKGLEWWARIRSKYNNYATYYADX₇VKX₈RFTISRDDSX₉X₁₀X₁₁X₁₂YMQMNNLKTEDTAX₁₃YYCVRHX₁₄NFGNSYX₁₅SX₁₆X₁₇AYWGQGTLLVTVSX₁₈, where X₁ is Q or K; X₂ is V or L; X₃ is V or E; X₄ is G or K; X₅ is K, V, S, G, R, T, or I; X₆ is M or I; X₇ is S or Q; X₈ is D, G, K, S, or E; X₉ is K or Q; X₁₀ is N or S; X₁₁ is T or I; X₁₂ is A or L; X₁₃ is V or M; X₁₄ is G, R or A; X₁₅ is I, L, V, or T; X₁₆ is Y, W or F; X₁₇ is W, F or Y; and X₁₈ is S or A; and
- ii) the VL region comprises the sequence of QX₁VVTQEX₂X₃LTX₄SPGX₅TVTLTCX₆SSTGAVTX₇X₈X₉YX₁₀NWVQX₁₁KPX₁₂X₁₃X₁₄X₁₅X₁₆GLIGX₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂GX₂₃PARFSGSLX₂₄GX₂₅KAALT₂₆X₂₇GX₂₈QX₂₉EDEAX₃₀YX₃₁CX₃₂LWYSNX₃₃VWFGGGTKLTVL, where X₁ is T or A; X₂ is P or S; X₃ is S or A; X₄ is V or T; X₅ is G or E; X₆ is G, R, or A; X₇ is S or T; X₈ is G or S; X₉ is N or Y; X₁₀ is P or A; X₁₁ is Q or E; X₁₂ is G or D; X₁₃ is Q or H; X₁₄ is A or L; X₁₅ is P or F; X₁₆ is R or T; X₁₇ is G or A; X₁₈ is K or D; X₁₉ is F or M; X₂₀ is L or R; X₂₁ is

A, P or V; X₂₂ is P or S; X₂₃ is T or V; X₂₄ is L or I; X₂₅ is G or D; X₂₆ is L or I; X₂₇ is S or T; X₂₈ is V or A; X₂₉ is P or T; X₃₀ is E or I; X₃₁ is Y or F; X₃₂ is V, A, or T; X₃₃ is R or L; and

- iii) wherein the VH and/or VL region sequence comprises one amino acid substitution or a combination thereof selected from
- a. N30, X₆34V, X₆34F, Q39, L45, D64, X₇65A, X₁₂81V, X₁₂81T, X₁₂81I, V99, H101, X₁₄102E, F104, and N106 in the VH region sequence in i); and
 - b. L20, V38, X₁₁40R, X₁₁40K, X₂₄69, X₃₂91L, X₃₃93, and G102 in the VL region sequence in ii).

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6. The polypeptide or polypeptide construct of claim 5, wherein in addition to said one amino acid substitution or a combination thereof as defined in iii) X₆ is I; X₈ is G; X₁₂ is L, X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence.

- 15 7. The polypeptide or polypeptide construct of claim 5 or 6, comprising combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more amino acid substitutions.

8. The polypeptide or polypeptide construct of any one of claims 5 to 7, wherein:

- 20 i) said one acid substitution is selected from
 - a. X₆34V, Q39E, Q39K, Q39R, Q39D, L45M, L45V, X₁₂81V, X₁₂81T, X₁₂81I, V99A, V99L, H101A, H101N in the VH region; and
 - b. V38I, V38L, V38M, V38F, V38Y, X₁₁40R, X₁₁40K, X₂₄69S, X₂₄69E, X₃₂91L, X₃₃93Y;
- 25 ii) said combination of two or more amino acid substitutions are selected from X₆34F and X₁₂81V in the VH region; Q39E in the VH region and X₁₁40K in the VL region; Q39E in the VH region and X₁₁40R in the VL region; Q39D in the VH region and X₁₁40K in the VL region; Q39D in the VH region and X₁₁40R in the VL region; L45V in the VH region and V38F in the VL region; L45V in the VH region and V38Y in the VL region; L45M in the VH region and X₁₁40K in the VL region; L20I and G102S in the VL region; X₁₂81V in the VH region and X₁₁40K in the VL region;
- 30 iii) said combination of three or more amino acid substitutions are selected from Q39E in the VH region, X₁₁40K and G102S in the VL region; Q39E in the VH region, X₁₁40R and G102S in the VL region; Q39D in the VH region, X₁₁40K and G102S in the VL region; Q39D in the VH region, X₁₁40R and G102S in the VL region; L45M in the VH region, X₁₁40K and G102S in the VL region; X₇65A, H101A, and N106S in the VH region; L20I, X₁₁40K, and G102S in the VL region;
- 35

- iv) said combination of four or more amino acid substitutions are selected from Q39E in the VH region, L20I, X₁₁40K and G102S in the VL region; Q39E in the VH region, L20I, X₁₁40R and G102S in the VL region; Q39D in the VH region, L20I, X₁₁40K and G102S in the VL region; Q39D in the VH region, L20I, X₁₁40R and G102S in the VL region; L45M in the VH region, L20I, X₁₁40K and G102S in the VL region; L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₁₂81V in the VH region, L20I, X₁₁40K, and G102S in the VL region;
- v) said combination of five, six, seven, eight, nine, ten, or more amino acid substitutions are selected from X₇65A, X₁₂81V, V99A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; D64E, X₇65A, X₁₂81V, X₁₄102E, F104I, N106T in the VH region, L20I, X₂₄69S, and G102S in the VL region; L45M, X₇65A, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₇65A, X₁₂81V, V99A, H101A, F104I, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₇65A, X₁₂81V, V99A, H101A, N106S in the VH region; X₁₂81V, V99A in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; Q39E, X₁₂81V in the VH region, L20I, X₁₁40K, and G102S in the VL region; L45V in the VH region, L20I, V38F, X₁₁40K and G102S in the VL region.
9. The polypeptide or polypeptide construct of any one of claims 5 to 8, wherein said combination of amino acid substitutions is selected from:
- ii) in the VH region
- X₇65A, X₁₂81V, V99A, H101A and N106S;
 - D64E, X₇65A, A81V, H101N, X₁₄102E, F104I, and N106S;
 - L45M, X₇65A, H101A, and N106T;
 - L45M, X₇65A, H101A, and N106S;
 - Q39E, X₇65A, H101N, and N106T;
 - D64E, X₇65A, V99A, H101A, and N106T;
 - X₇65A, X₁₂81V, V99A, H101A, X₁₄102E, F104I, and N106T;
 - X₇65A, X₁₂81V, H101N, X₁₄102E, F104I, and N106S;
 - D64E, X₇65A, X₁₂81V, H101A, and N106S;
 - D64E, X₇65A, H101A, and N106T;
 - X₇65A, V99A, H101A, and N106T;
 - D64E, X₇65A, H101A, and N106S;
 - D64E, X₇65A, X₁₂81V, V99A, H101A, and N106S;
 - X₇65A, H101A and N106S;
 - N30S, Q39E, D64E, X₇65A, X₁₂81V, H101A, X₁₄102E, F104I, and N106T;

- p. L45M, D64E, X₇65A, H101A, and N106T;
- q. N30S, L45M, X₇65A, X₁₂81V, H101A, and N106T;
- r. N30S, L45M, D64E, X₇65A, X₁₂81V, H101A, and N106S;
- iii) in the VL region
 - 5 a. L20I, X₁₁40K, X₂₄69S, and G102S;
 - b. L20I, X₂₄69S, and G102S;
 - c. L20I, V38I, X₁₁40K, X₂₄69E, G102S and X₃₃93Y;
 - d. X₁₁40K and G102S;
 - e. L20I, X₁₁40K, X₂₄69S, G102S and X₃₃93Y;
 - 10 f. L20M, X₁₁40K and X₂₄69E;
 - g. L20I, V38I, X₁₁40K, X₂₄69E and G102S;
 - h. X₁₁40K, X₂₄69S and X₃₃93Y; or
 - i. X₁₁40K and X₂₄69S; and
 - iv) a combination of one amino acid substitution combination of i) and ii).
- 15 10. The polypeptide or polypeptide construct of claim 9, wherein said combination of amino acid substitution combinations of iii) is selected from:
 - a. X₇65A, X₁₂81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
 - 20 b. D64E, X₇65A, X₁₂81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
 - c. L45M, X₇65A, H101A, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
 - d. L45M, X₇65A, H101A, N106S in the VH region, L20I, V38I, X₁₁40K, X₂₄69E, G102S and X₃₃93Y in the VL region;
 - 25 e. Q39E, X₇65A, H101N, N106T in the VH region, X₁₁40K and G102S in the VL region;
 - f. D64E, X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
 - 30 g. X₇65A, X₁₂81V, V99A, H101A, X₁₄102E, F104I, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
 - h. X₇65A, X₁₂81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
 - i. D64E, X₇65A, X₁₂81V, H101A, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
 - 35 j. D64E, X₇65A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;

- k. X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- l. D64E, X₇65A, H101A, N106S in the VH region, X₁₁40K and G102S in the VL region;
- 5 m. D64E, X₇65A, X₁₂81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, G102S and X₃₃93Y in the VL region;
- n. X₇65A, H101A, N106S in the VH region, X₁₁40K and G102S in the VL region;
- o. N30S, Q39E, D64E, X₇65A, X₁₂81V, H101A, X₁₄102E, F104I, N106T in the VH region, L20M, X₁₁40K and X₂₄69E in the VL region;
- 10 p. L45M, D64E, X₇65A, H101A, N106T in the VH region, L20I, V38I, X₁₁40K, X₂₄69E and G102S in the VL region;
- q. N30S, L45M, X₇65A, X₁₂81V, H101A, N106T in the VH region, X₁₁40K and X₂₄69S in the VL region; and
- r. N30S, L45M, D64E, X₇65A, X₁₂81V, H101A, N106S in the VH region, X₁₁40K and
15 X₂₄69S in the VL region.
11. The polypeptide or polypeptide construct of claim 10, wherein in said combination of amino acid substitution combinations defined in:
- a. and m. X₆ is I in said VH region sequence;
- 20 b. and r. X₈ is G in said VH region sequence;
- c. X₁₂ is L in said VH region;
- d. X₁₂ is L and X₁₇ is F in said VH region;
- e. X₆ is I, X₁₄ is A and X₁₇ is F in said VH region sequence;
- f. X₅ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
- 25 g. X₅ is I in said VH region sequence;
- h. and i. X₈ is G in said VH region sequence;
- j., l. and n. X₆ is I and X₁₇ is F in said VH region sequence; and X₃₂ is A in said VL region sequence;
- k. X₆ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
- 30 p. X₁₂ is L in said VH region; and
- q. X₈ is G and X₁₇ is F in said VH region sequence.
12. The polypeptide or polypeptide construct of claim 5, or any one of claims 6 to 11, wherein said VH and VL region of i) and ii) is selected from the VH and VL region combinations as defined in SEQ ID NOs: 124 and 125, 172 and 173, 362 and 363, 552 and 553, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855, wherein said one amino acid substitution or a
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combination thereof in said VH and/or VL region sequence results in a VH and/or a VL region sequence having the amino acid residue:

- i. I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, and S at position 102 in the VL region sequence;
M at position 45, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
M at position 45, A at position 65, L at position 81, A at position 101, S at position 106, F at position 112 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69, S at position 102 and Y at position 93 in the VL region sequence;
I at position 34, E at position 39, A at position 65, N at position 101, A at position 102, T at position 106, F at position 112 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, A at position 99, A at position 101, T at position 106 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, S at position 102 and Y at position 93 in the VL region sequence;
I at position 34, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S

- at position 102 in the VL region sequence;
- M at position 45, E at position 64, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69 and S at position 102 in the VL region sequence;
- 5 S at position 30, M at position 45, A at position 65, G at position 68, V at position 81, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, S at position 69 and Y at position 93 in the VL region sequence; and
- 10 S at position 30, M at position 45, E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, K at position 40 and S at position 69 in the VL region sequence;
- ii. E at position 64, A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;
- 15 A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, S at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;
- 20 I at position 34, A at position 65, A at position 99, A at position 101, T at position 106 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence; and
- S at position 30, E at position 39, E at position 64, A at position 65, V at position 81, A at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, M at position 20, K at position 40 and E at position 69 in the VL region sequence;
- 25 iii. A at position 101 in the VH region sequence;
- iv. V at position 81, A at position 99 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
- 30 I at position 34, V at position 81 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;
- I at position 34 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;
- 35 I at position 34, E at position 39, V at position 81 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

- v. I at position 34,_V at position 81 in the VH region sequence, and K at position 40 in the VL region sequence;
M at position 45 in the VH region sequence,_I at position 20,_K at position 40 and _S at position 102 in the VH region sequence;
- 5 I at position 34,_A at position 65,_A at position 101 and _S at position 106S in the VH region sequence;
I at position 20,_K at position 40,_S at position 69 and _S at position 102 in the VL region sequence;
F at position 34_and V at position 81 in the VH region sequence;
- 10 M at position 45 in the VH region sequence, K at position 40 and _S at position 102 in the VL region sequence;
D at position 39 in the VH region sequence, I at position 20,_K at position 40 and S at position 102 in the VL region sequence;
I at position 34_and V at position 81 in the VH region sequence;
- 15 E at position 39 in the VH region sequence, I at position 20,_K at position 40 and _S at position 102 in the VL region sequence;
M at position 45 in the VH region sequence_and_K at position 40 in the VL region sequence;
I at position 34,_A at position 65,_V at position 81,_A at position 99,_A at position 101_and S at position 106 in the VH region sequence; or
- 20 vi. D at position 39 in the VH region sequence,_I at position 20,_R at position 40 and _S at position 102 in the VL region sequence;
I at position 34 in the VH region sequence;
K at position 40 in the VL region sequence;
- 25 D at position 39_in the VH region sequence, K at position 40 and _S at position 102 in the VL region sequence;
I at position 20 and _S at position 102 in the VH region sequence;
K at position 39 in the VH region sequence;
E at position 39 in the VH region sequence,_K at position 40_and S at position 102 in the VL region sequence;
- 30 E at position 39 in the VH region sequence,_I at position 20,_R at position 40_and S at position 102 in the VL region sequence;
D at position 39_in the VH region sequence,_R at position 40_and S at position 102 in the VL region sequence;
- 35 V at position 81 in the VH region sequence;
D at position 39 in the VH region sequence and_K at position 40 in the VL region sequence;

F at position 112 in the VH region sequence;

F at position 112 in the VH region sequence and_I at position 38 in the VL region sequence;

5 E at position 39 in the VH region sequence and K at position 40 in the VL region sequence;

V at position 34 in the VH region sequence.

13. The polypeptide or polypeptide construct of any one of claims 1 to 12, wherein the VH and VL region sequence are linked by a linker.

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14. The polypeptide or polypeptide construct of claim 13, wherein the linker is a peptide linker.

15. The polypeptide or polypeptide construct of claim 14, wherein said peptide linker comprises or consists of a G₄S linker, or G₄Q linker or repetitions thereof.

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16. The polypeptide or polypeptide construct of any one of claims 1 to 15, wherein the polypeptide or polypeptide construct comprises at least one further binding domain.

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17. The polypeptide or polypeptide construct of claim 16, wherein said at least one further binding domain binds to a cell surface antigen.

18. The polypeptide or polypeptide construct of claim 17, wherein said cell surface antigen is a tumor antigen.

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19. The polypeptide or polypeptide construct of claim 18, wherein the tumor antigen is selected from the group consisting of BCMA, CD123, CD19, CD20, CD22, CD33, CD70, CDH19, CDH3, CLL1, CS1, CLDN6, CLDN18.2, DLL3, EGFRvIII, FLT3, MAGEB2, MART1, MSLN, MUC17, PSMA, and STEAP1.

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20. The polypeptide or polypeptide construct of any one of claims 1 to 19, wherein said polypeptide or polypeptide construct is a single chain polypeptide that is at least bispecific.

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21. A polynucleotide encoding a polypeptide or polypeptide construct as defined in any one of claims 1 to 20.

22. A vector comprising a polynucleotide as defined in claim 21.
23. A host cell transformed or transfected with the polynucleotide as defined in claim 21 or with the vector as defined in claim 22.
- 5 24. A process for the production of an polypeptide or polypeptide construct according to any one of claims 1 to 20, said process comprising culturing a host cell as defined in claim 23 under conditions allowing the expression of the polypeptide or polypeptide construct as defined in any one of claims 1 to 20 and recovering the produced polypeptide or
- 10 polypeptide construct from the culture.
25. A pharmaceutical composition comprising a polypeptide or polypeptide construct according to any one of claims 1 to 20, or produced according to the process of claim 24.
- 15 26. The polypeptide or polypeptide construct of any one of claims 18 to 20, or produced according to the process of claim 24, for use in the prevention, treatment or amelioration of a disease selected from a tumorous disease.
- 20 27. A method for the prevention, treatment or amelioration of a tumorous disease, comprising administering to a subject in need thereof the polypeptide or polypeptide construct according to any one of claims 18 to 20, or produced according to the process of claim 24.
- 25 28. A kit comprising a polypeptide or polypeptide construct according to any one of claims 1 to 20, or produced according to the process of claim 24, a polynucleotide as defined in claim 21, a vector as defined in claim 22, and/or a host cell as defined in claim 23.